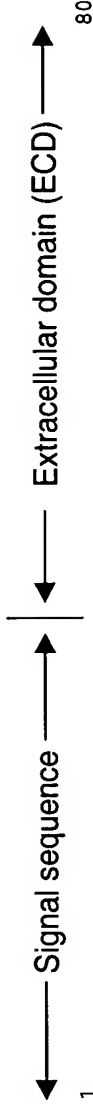


Fig. 1



SEQ: 278_Human_B7-1

SEQ: 048_R1_Clone_71
SEQ: 049_R1_Clone_84
SEQ: 050_R1_Clone_118
SEQ: 051_R1_Clone_126
SEQ: 052_R2_CD28BP-1
SEQ: 053_R2_CD28BP-2
SEQ: 054_R2_CD28BP-3
SEQ: 055_R2_CD28BP-4
SEQ: 056_R2_CD28BP-5
SEQ: 057_R2_CD28BP-6
SEQ: 058_R2_CD28BP-7
SEQ: 059_R2_CD28BP-8
SEQ: 060_R2_CD28BP-9
SEQ: 061_R2_CD28BP-10
SEQ: 062_R2_CD28BP-11
SEQ: 063_R2_CD28BP-12
SEQ: 064_R2_CD28BP-13
SEQ: 065_R2_CD28BP-14
SEQ: 066_R2_CD28BP-15
SEQ: 067_R2_CD28BP-16
SEQ: 068_R2_CD28BP-17

SEQ: 174_cd28A12-5
SEQ: 175_cd28A4-5star
SEQ: 176_cd28A4-9
SEQ: 177_cd28A6-9
SEQ: 178_cd28A6-1
SEQ: 179_cd28A8-4
SEQ: 180_cd28A8-6
SEQ: 181_cd28B2-8
SEQ: 182_cd28B4-3
SEQ: 183_cd28B6-3
SEQ: 184_cd28B6-6
SEQ: 185_cd28B8-5star

SEQ: 186_cd28C11-5

Fig. 2A

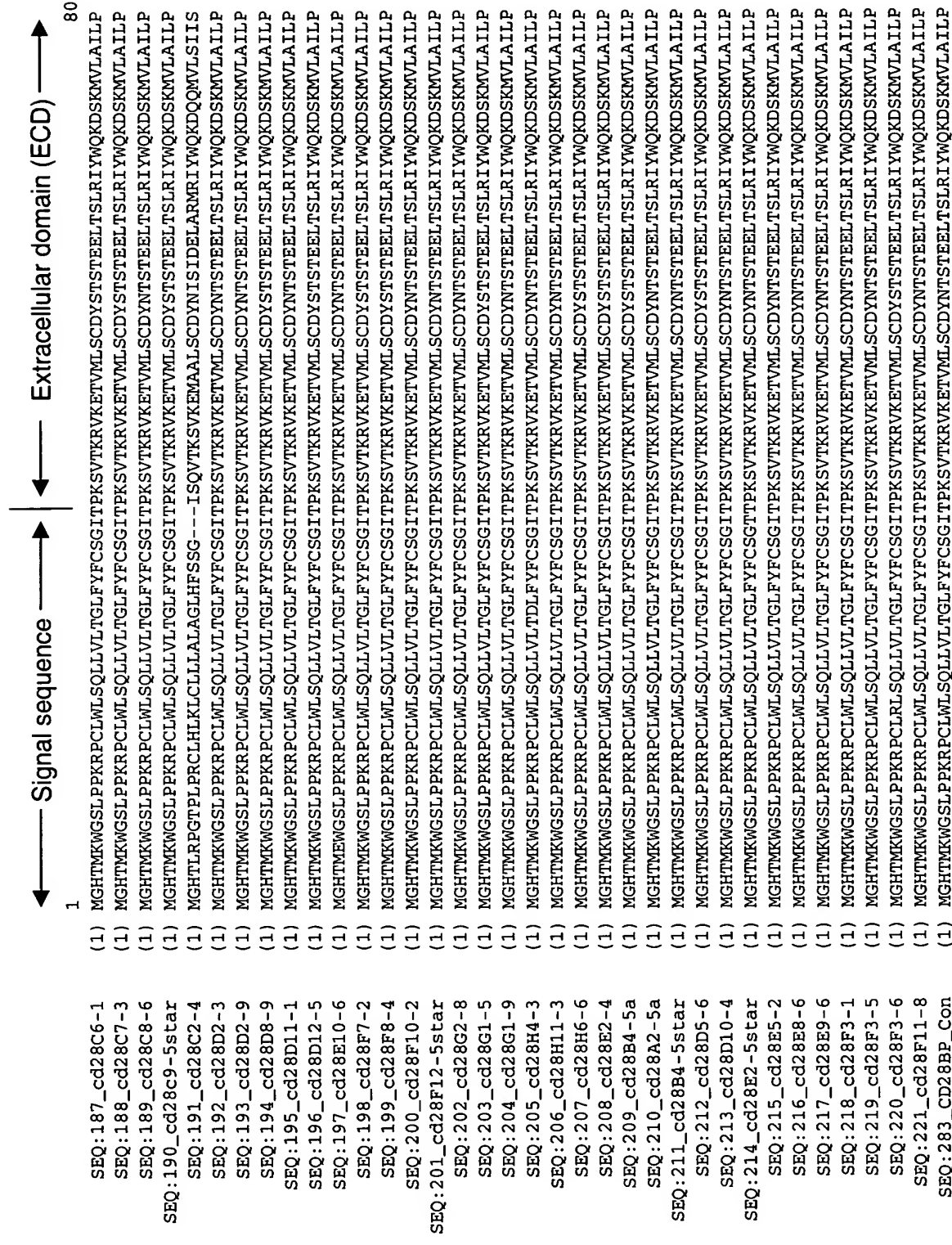


Fig. 2B

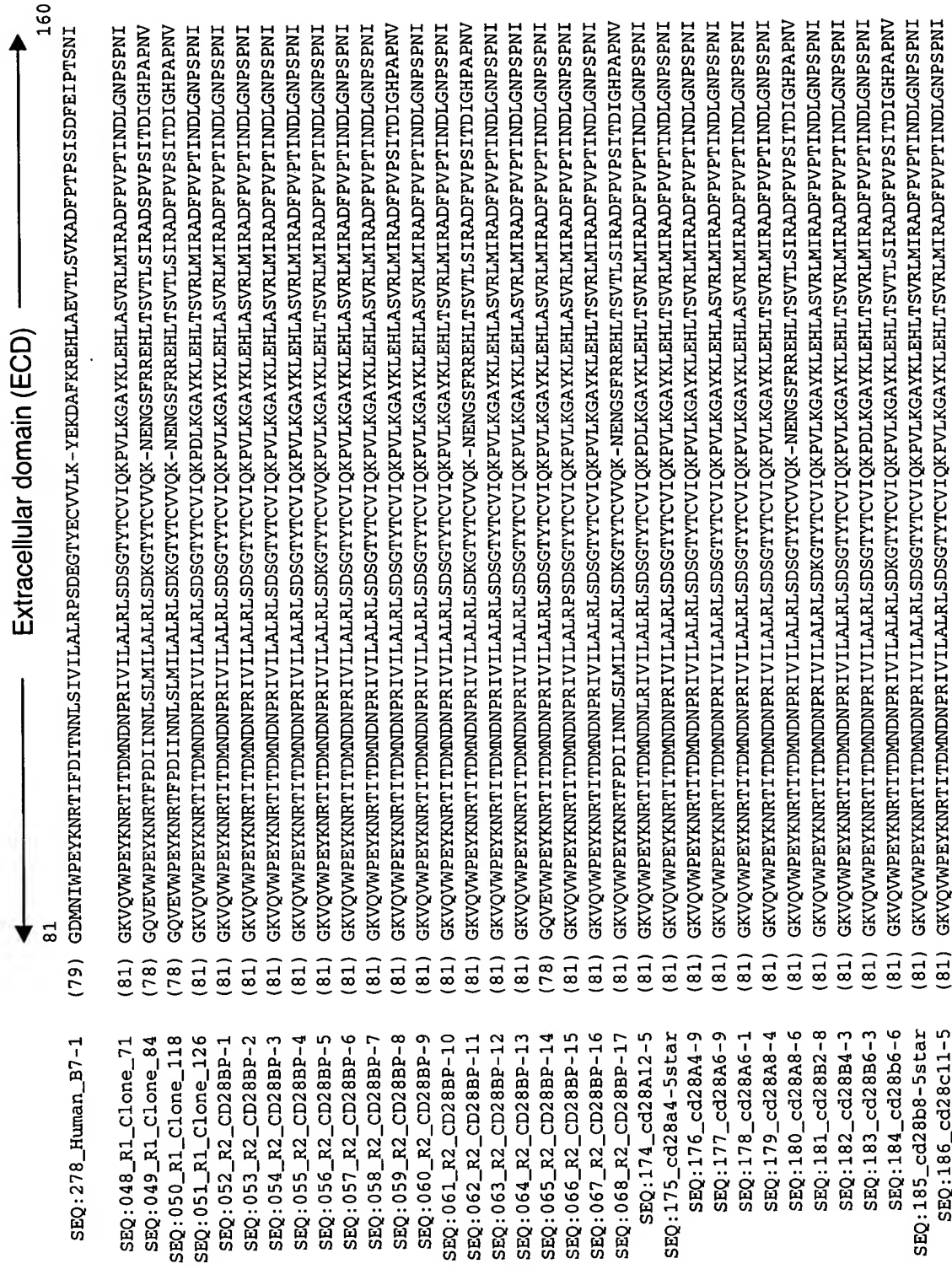


Fig. 2C

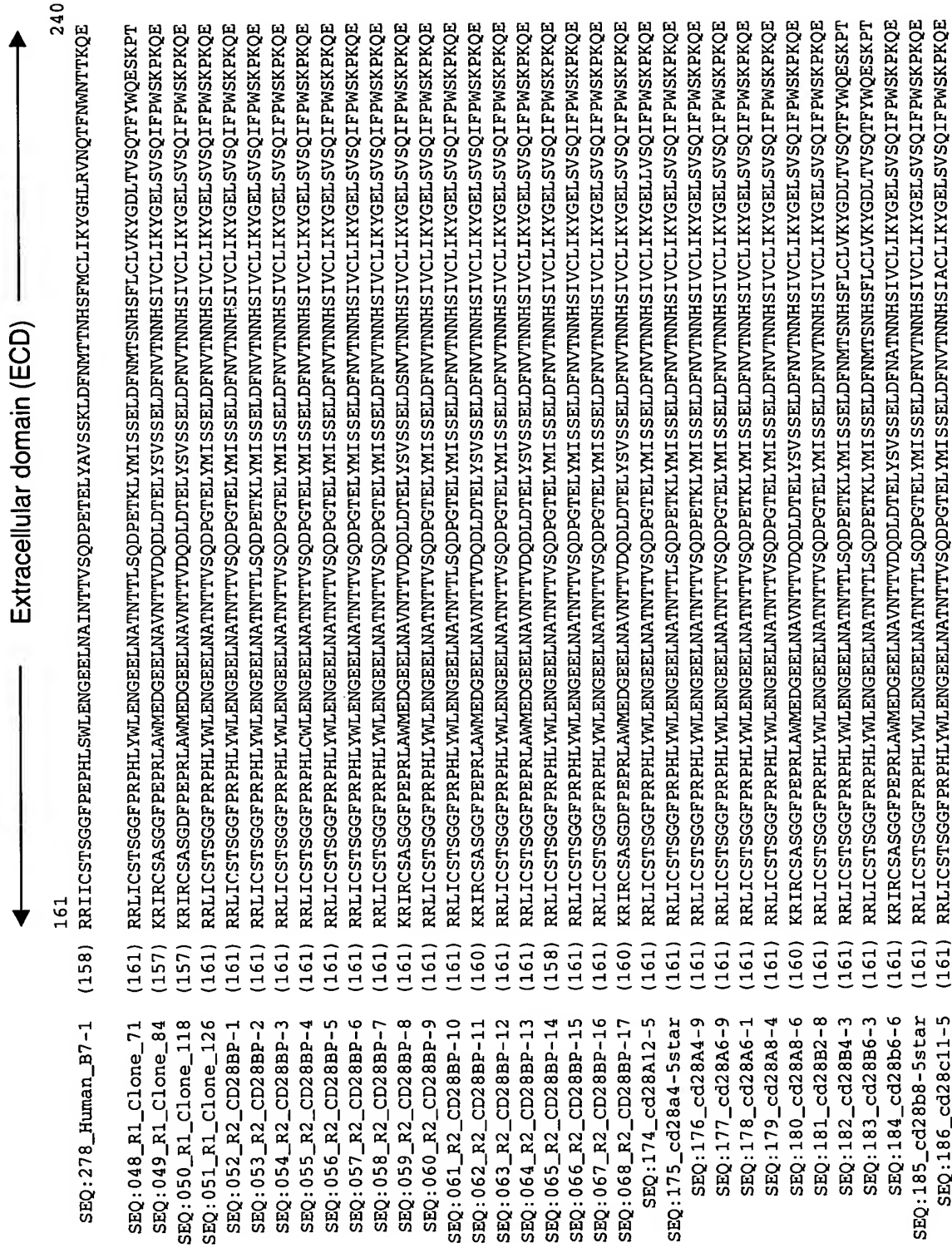


Fig. 2E

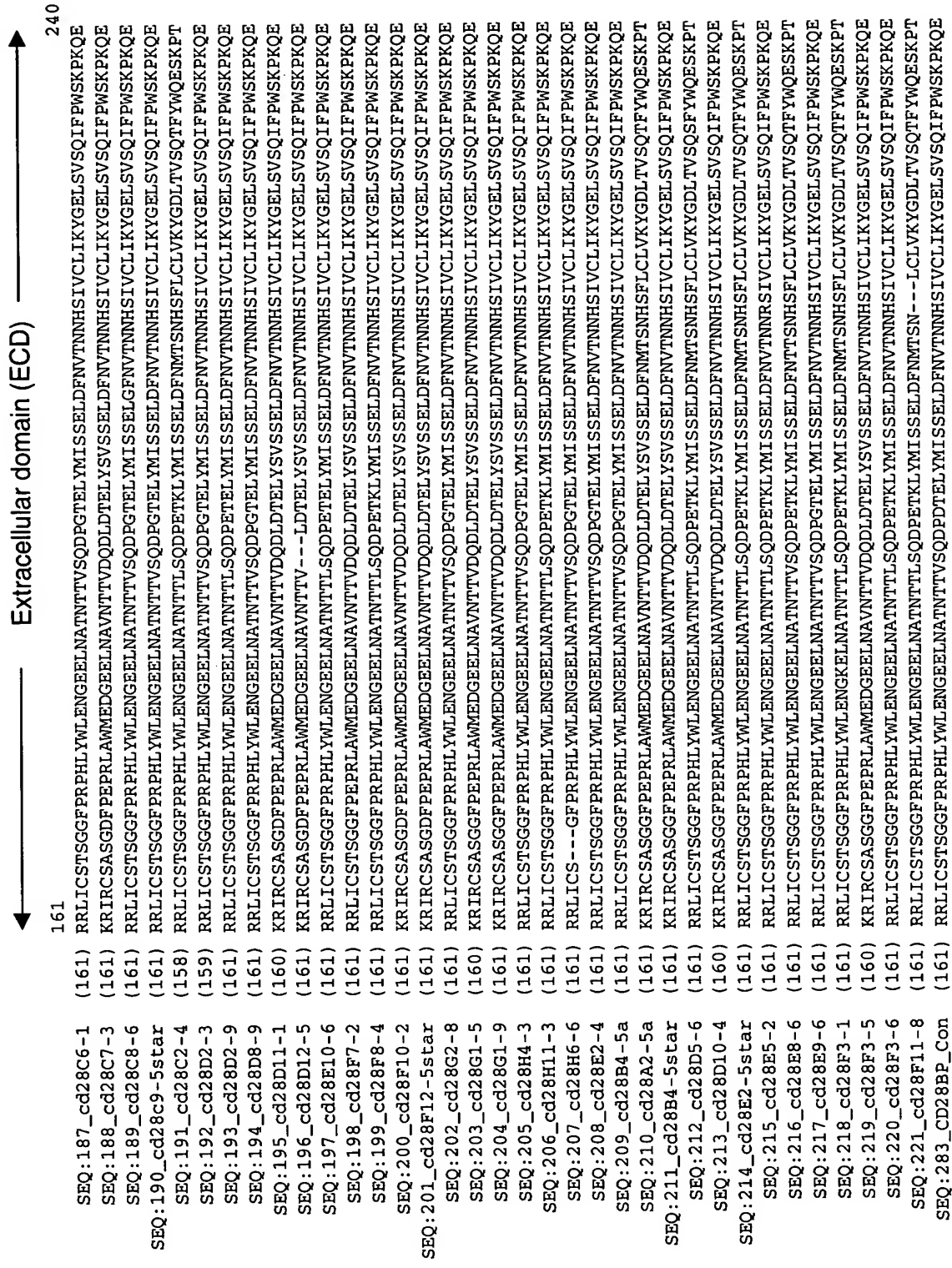


Fig. 2F

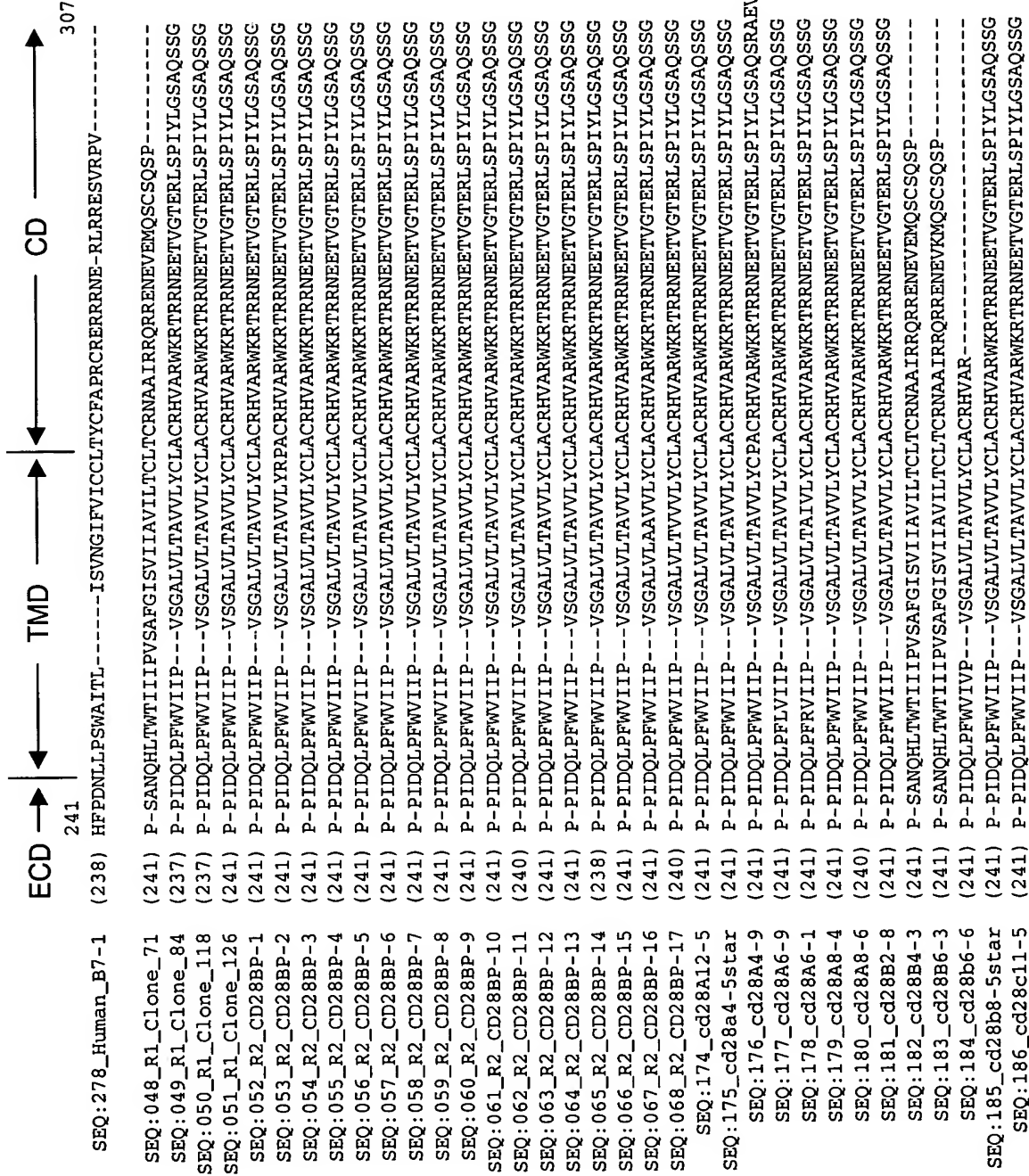


Fig. 2G

		ECD →	← TMD	←	← CD	←	
		241					307
SEQ:187_cd28C6-1	(241)	P-PIDQLPFWVIIP	---	VSGALVLTAVVLYCLACRHGARMKTRRNEETVGT	RLSPIYLGSAQSSG		
SEQ:188_cd28C7-3	(241)	P-PIDQLPFWVIIP	---	VSGALVLTAVVLYCLACRHVARWKTRRNEETVGT	RLSPIYLGSAQSSG		
SEQ:189_cd28C8-6	(241)	P-PIDQLPFWVIIP	---	VSGALVLTAVVLYCLACRHVARWKTRRNEETVGT	RLSPIYLGSAQSSG		
SEQ:190_cd28C9-5star	(241)	P-PIDQLPFWVIIP	---	VSGALVLTAVVLYCLACRHVARXKTRRNEETVGT	RLSPIYLGSAQSSG		
SEQ:191_cd28C2-4	(238)	P-SANQHLTWIIIP	VPVS	AFGISVIAVILTCLTCR	NAAIRRQRRENEVEMQSCSQSP	-----	
SEQ:192_cd28D2-3	(239)	P-PIDQLPFWVIIP	---	VSGALVLTAVVLYCLACRHVARWKTRRNEETVGT	RLSPIYLGSAQSSG		
SEQ:193_cd28D2-9	(241)	P-PIDQLPFWVIIP	---	VSGALVLTAVVLYCLACRHVARWKTRRNEETVGT	RLSPIYLGSAQSSG		
SEQ:194_cd28D8-9	(241)	P-PIDQLPFWVIIP	---	VSGALVLTAVVLYCLACRHVARWKTRRNEETVGT	RLSPIYLGSAQSSG		
SEQ:195_cd28D11-1	(240)	P-PIDQLPFWVIIP	---	VSGALVLTAVVLYCLACRHVARWKTRRNEETVGT	RLSPIYLGSAQSSG		
SEQ:196_cd28D12-5	(238)	P-PIDQLPFWVIIP	---	VSGALVLTAVVLYCLACRHVARWKTRRNEETVGT	RLSPIYLGSAQSSG		
SEQ:197_cd28E10-6	(241)	P-PIDQLPFWVIIP	---	VSGALVLTAVVLYCLACRHVARWKTRRNEETVGT	RLSPIYLGSAQSSG		
SEQ:198_cd28F7-2	(241)	P-PIDQLPFWVIIP	---	VSGALVLTAVVLYCLACRHVARWKTRRNEETVGT	RLSPIYLGSAQSSG		
SEQ:199_cd28F8-4	(241)	P-PIDQLPFWVIIP	---	VSGALVLTAVVLYCLACRHVARWKTRRNEETVGT	RLSPIYLGSAQSSG		
SEQ:200_cd28F10-2	(241)	P-PIDQLPFWVIIP	---	VSGALVLTAVVLYCLACRHVARWKTRRNEETVGT	RLSPIYLGSAQSSG		
SEQ:201_cd28F12-5star	(241)	P-PIDQLPFWVIIP	---	VSGALVLTAVVLYCLACRHVARWKTRRNEETVGT	RLSPIYLGSAQSSG		
SEQ:202_cd28G2-8	(241)	P-PIDQLPFWVIIP	---	VSGALVLTAVVLYCLACRHVARWKTRRNEETVGT	RLSPIYLGSAQSSG		
SEQ:203_cd28G1-5	(240)	P-PIDQLPFWVIIP	---	VSGALVLTAVVLYCLACRHVARWKTRRNEETVGT	RLSPIYLGSAQSSG		
SEQ:204_cd28G1-9	(241)	P-PIDQLPFWVIIP	---	VSGALVLTAVVLYCLACRHVARWKTRRNEETVGT	RLSPIYLGSAQSSG		
SEQ:205_cd28H4-3	(241)	P-PIDQLPFWVIIP	---	VSGALVLTAVVLYCLACRHVARWKTRRNEETVGT	RLSPIYLGSAQSSG		
SEQ:206_cd28H11-3	(241)	P-PIDQLPFWVIIP	---	VSGALVLTAVVLYCLACRHVARWKTRRNEETVGT	RLSPIYLGSAQSSG		
SEQ:207_cd28H6-6	(238)	P-PIDQLPFWVIIP	---	VSGALVLTAVVLYCLACRHVARWKTRRNEETVGT	RLSPIYLGSAQSSG		
SEQ:208_cd28E2-4	(241)	P-PIDQLPFWVIIP	---	VSGALVLTAVVLYCLACRHVARWKTRRNEETVGT	RLSPIYLGSAQSSG		
SEQ:209_cd28B4-5a	(241)	P-PIDQLPFWVIIP	---	VSGALVLTAVVLYCLACRHVARWKTRRNEETVGT	RLSPIYLGSAQSSG		
SEQ:210_cd28A2-5a	(241)	P-SANQHLTWIIIP	VPVS	AFGISVIAVILTCLTCR	NAAIRRQRRENEGCKVLSVIGTKLKFN	---	
SEQ:211_cd28B4-5star	(241)	P-PIDQLPFWVIIP	---	VSGALVLTAVVLYCLACRHVARWKTRRNEETVGT	RLSPIYLGSAQSSG		
SEQ:212_cd28D5-6	(241)	P-SANQHLTWIIIP	VPVS	AFGISVIAVILTCLTCR	NAAIRRQRRENEVEMQSCSQSP	-----	
SEQ:213_cd28D10-4	(240)	P-PIDQLPFWVIIP	---	VSGALVLTAVVLYCLACRHVARWKTRRNEETVGT	RLSPIYLGSAQSSG		
SEQ:214_cd28E2-5star	(241)	P-SANQHLTWIIIP	VPVS	AFGISVIAVILTCLTCR	NAAIRRQRRENEVEMQSCSQSP	-----	
SEQ:215_cd28E5-2	(241)	P-PIDQLPFWVIIP	---	VSGALVLTAVVLYCLACRHVARWKTRRNEETVGT	RLSPIYLGSAQSSG		
SEQ:216_cd28E8-6	(241)	P-SANQHLTWIIIP	VPVS	AFGISVIAVILTCLTCR	NAAIRRQRRENEVEMQSCSQSP	-----	
SEQ:217_cd28E9-6	(241)	P-PIDQLPFWVIIP	---	VSGALVLTAVVLYCLACRHVARWKTRRNEETVGT	RLSPIYLGSAQSSG		
SEQ:218_cd28F3-1	(241)	P-SANQHLTWIIIP	VPVS	AFGISVIAVILTCLTCR	NAAIRRQRRENEVEMQSCSQSP	-----	
SEQ:219_cd28F3-5	(240)	P-PIDQLPFWVIIP	---	VSGALVLTAVVLYCLACRHVARWKTRRNEETVGT	RLSPIYLGSAQSSG		
SEQ:220_cd28F3-6	(241)	P-PIDQLPFWVIIP	---	VSGALVLTAVVLYCLACRHVARWKTRRNEETVGT	RLSPIYLGSAQSSG		
SEQ:221_cd28F11-8	(238)	P-SANQHLTWIIIP	VPVS	AFGISVIAVILTCLTCR	NAAIRRQRRENEVEMQSCSQSP	-----	
SEQ:283_CD28BP_Con	(241)	P	PIDQLPFWVIIP	---	VSGALVLTAVVLYCLACRHVARWKTRRNEETVGT	RLSPIYLGSAQSSG	

Fig. 2H



80

SEQ: 278_Human_B7-1	(1) MGHTRRQGTSPSKCPYLNFQQLLVLAGLSHFCSGVIHVTKEVEKAVATLSCGHNVSVEELAQTRIYWQKEKKMVLTTMMSGD
SEQ: 069_R1_CTLA4BP-5	(1) MGHTRRQGTSPSKCPYLKFFQQLLVLAGLSHFCSGVIHVTKEVEKAVATLSCGHNVSVEELAQTRIHWQKEKKMVLTTMMSGD
SEQ: 070_R1_CTLA4BP-7	(1) MGHTRRQGTSPSKCPYLKFFQQLLVLAGLSHFCSGVIHVTNEVEKAVATLSCGHNVSVEELAQTRIYWQKEKKMVLTTMMSGD
SEQ: 071_R1_CTLA4BP-11	(1) MSHTRRQGTSPSKCPYLKFFQQLLVLAGLSHFCSGVIHMTKEVEKAVATLSCGHNVSVEELAQTRIYWQKEKKMVLTTMMSGD
SEQ: 072_R1_CTLA4BP-13	(1) MGHTRRQGTSPSKCPYLKFFQQLLVLAGLSHFCSGVIHVTKEVEKAVATLSCGHNVSVEELAQTRIYWQKEKKMVLTTMMSGD
SEQ: 073_R1_CTLA4BP-27	(1) MSHTRRQGTSPSKCPYLNFQQLLVLAGLSHFCSGVIHVTKEVEKAVATLSCGHNVSVEELAQTRIYWQKEKKMVLTTMMSGD
SEQ: 074_R2_CTLA4BP-5x2-10c	(1) MGHTRRQGTSPSKCPYLNFQQLLVLAGLSHFCSGVIHVTKEVEKAVATLSCGHNVSVEELAQTRIYWQKEKKMVLTTMMSGD
SEQ: 075_R2_CTLA4BP-5x2-11d	(1) MSHTRRQGTSPSKCPYLKFFQQLLVLAGLSHFCSGVIHVTKEVEKAVATLSCGHNVSVEELAQTRIHWQKEKKMVLTTMMSGD
SEQ: 076_R2_CTLA4BP-5x2-12f	(1) MSHTRRQGTSPSKCPYLKFFQQLLVLAGLSHFCSGVIHVTKEVEKAVATLSCGHNVSVEELAQTRIHWQKEKKMVLTTMMSGD
SEQ: 077_R2_CTLA4BP-5x2-2g	(1) MSHTRRQGTSPSKCPYLKFFQQLLVLAGLSHFCSGVIHVTKEVEKAVATLSCGHNVSVEELAQTRIHWQKEKKMVLTTMMSGD
SEQ: 078_R2_CTLA4BP-5x2-3c	(1) MGHTRRQGTSPSKCPYLKFFQQLLVLAGLSHFCSGVIHVTKEVEKAVATLSCGHNVSVEELAQTRIHWQKEKKMVLTTMMSGD
SEQ: 079_R2_CTLA4BP-5x2-4c	(1) MGHTRRQGTSPSKCPYLKFFQQLLVLAGLSHFCSGVIHVTREVEKAVATLSCGHNVSVEELAQTRIHWQKEKKMVLTTMMSGD
SEQ: 080_R2_CTLA4BP-5x2-7b	(1) MSHTRRQGTSPSKCPYLKFFQQLLVLAGLSHFCSGVIHVTKEVEKAVATLSGGLNVSVEELAQTRIYWQKEKKMVLTTMMSGD
SEQ: 081_R2_CTLA4BP-5x2-8c	(1) MSHTRRQGTSPSKCPYLNFQQLLVLAGLSHFCSGVIHVTKEVEKAVATLSGHNVSVEELAQTRIHWQKEKKMVLTTMMSGD
SEQ: 082_R2_CTLA4BP-5x3-10e	(1) MSHTRRQGTSPSKCPYLKFFQQLLVLAGLSHFCSGVIHMTKEVEKAVATLSGHNVSVEELAQTRIYWQKEKKMVLTTMMSGD
SEQ: 083_R2_CTLA4BP-5x3-11b	(1) MGHTRRQGTSPSKCPYLKFFQQLLVLAGLSHFCSGVIHVTKEVEKAVATLSGHNVSVEELAQTRIYWQKEKKMVLTTMMSGD
SEQ: 084_R2_CTLA4BP-5x3-6f	(1) MSHTRRQGTSPSKCPYLKFFQQLLVLAGLSHFCSGVIHVTKEVEKAVATLSGHNVSVEELAQTRIYWQKEKKMVLTTMMSGD
SEQ: 085_R2_CTLA4BP-5x4-11d	(1) MGHTRRQGTSPSKCPYLNFQQLLVLAGLSHFCSGVIHVTKEVEKAVATLSGHNVSVEELAQTRIYWQKEKKMVLTTMMSGD
SEQ: 086_R2_CTLA4BP-5x4-12c	(1) MGHTRRQGTSPSKCPYLKFFQQLLVLAGLSHFCSGVIHVTKEVEKAVATLSGHNVSVEELAQTRIHWQKEKKMVLTTMMSGD
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SEQ: 089_R2_CTLA4BP-5x5-6e	(1) MGHTRRQGTSPSKCPYLKFFQQLLVLAGLSHFCSGVIHVTKEVEKAVATLSGHNVSVEELAQTRIHWQKEKKMVLTTMMSGD
SEQ: 090_R2_CTLA4BP-5x6-9d	(1) MGHTRRQGTSPSKCPYLKFFQQLLVLAGLSHFCSGVIHVTKEVEKAVATLSGGLNVSVEELAQTRIHWQKEKKMVLTTMMSGD
SEQ: 091_R2_CTLA4BP-5x8-1f	(1) MSHTRRQGTSPSKCPYLKFFQQLLVLAGLSHFCSGVIHVTKEVEKAVATLSGHNVSVEELAQTRIHWQKEKKMVLTTMMSGD
SEQ: 092_R2_CTLA4BP-5x9-12c	(1) MGHTRRQGTSPSKCPYLNFQQLLVLAGLSHFCSGVIHVTKEVEKAVATLSGHNVSVEELAQTRIHWQKEKKMVLTTMMSGD
SEQ: 222_ctla5x9d10	(1) MGHTRRQGTSPSKCPYLNFQQLLVLAGLSHFCSGVIHVTKEVEKAVATLSGHNVSVEELAQTRIHWQKEKKMVLTTMMSGD
SEQ: 223_ctla5x6f6	(1) MGHTRRQGTSPSKCPYLKFFQQLLVLAGLSHFCSGVIHVTKEVEKAVATLSGHNVSVEELAQTRIHWQKEKKMVLTTMMSGD
SEQ: 224_ctla5x5h12	(1) MSHTRRQGTSPSKCPYLKFFQQLLVLAGLSHFCSGVIHVTKEVEKAVATLSGGLNVSVEELAQTRIYWQKEKKMVLTTMMSGD
SEQ: 225_ctla5x5c10	(1) MGHTRRQGTSPSKCPYLNFQQLLVLAGLSHFCSGVIHVTKEVEKAVATLSGHNVSVEELAQTRIYWQKEKKMVLTTMMSGD

Fig. 3A

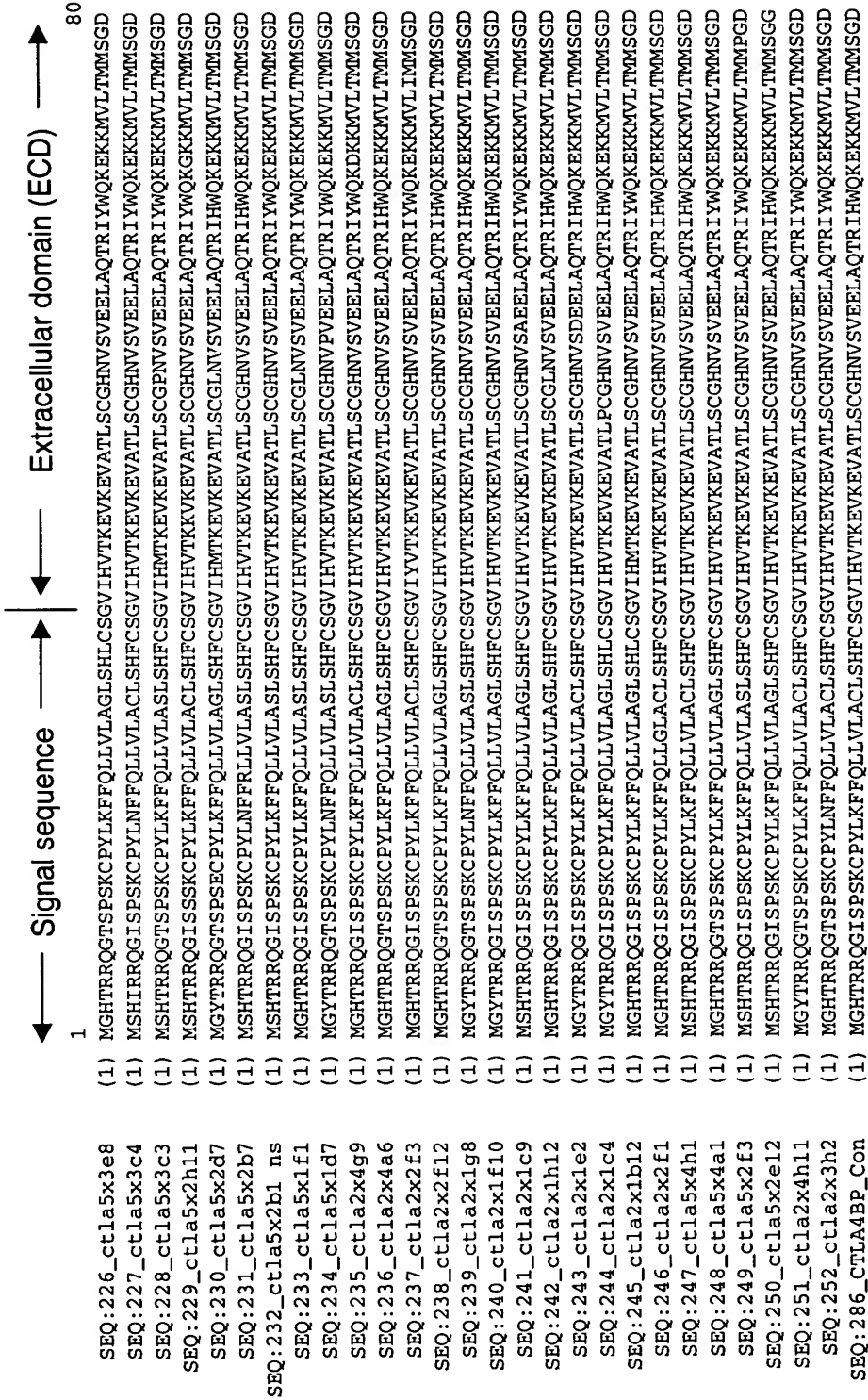
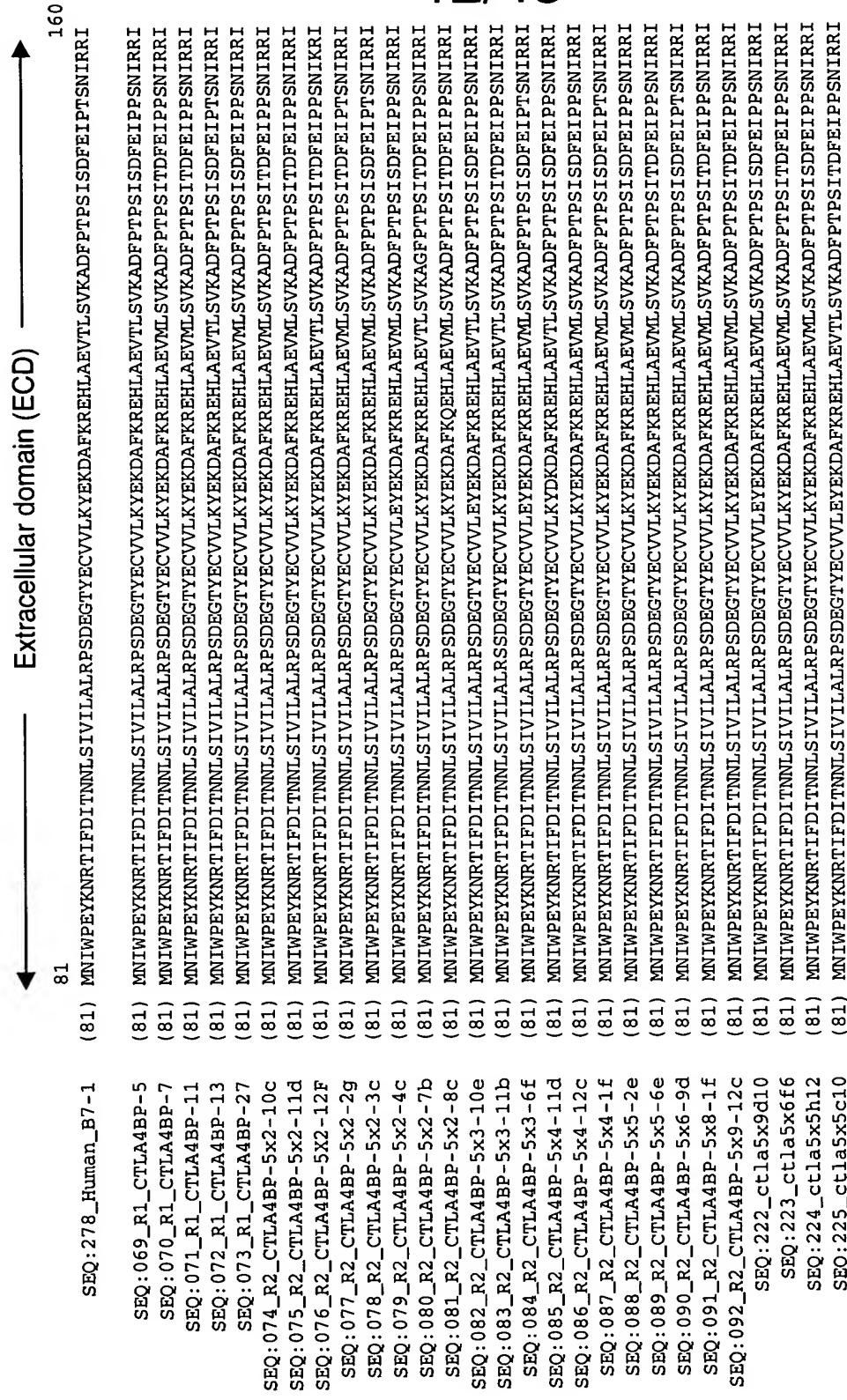


Fig. 3B



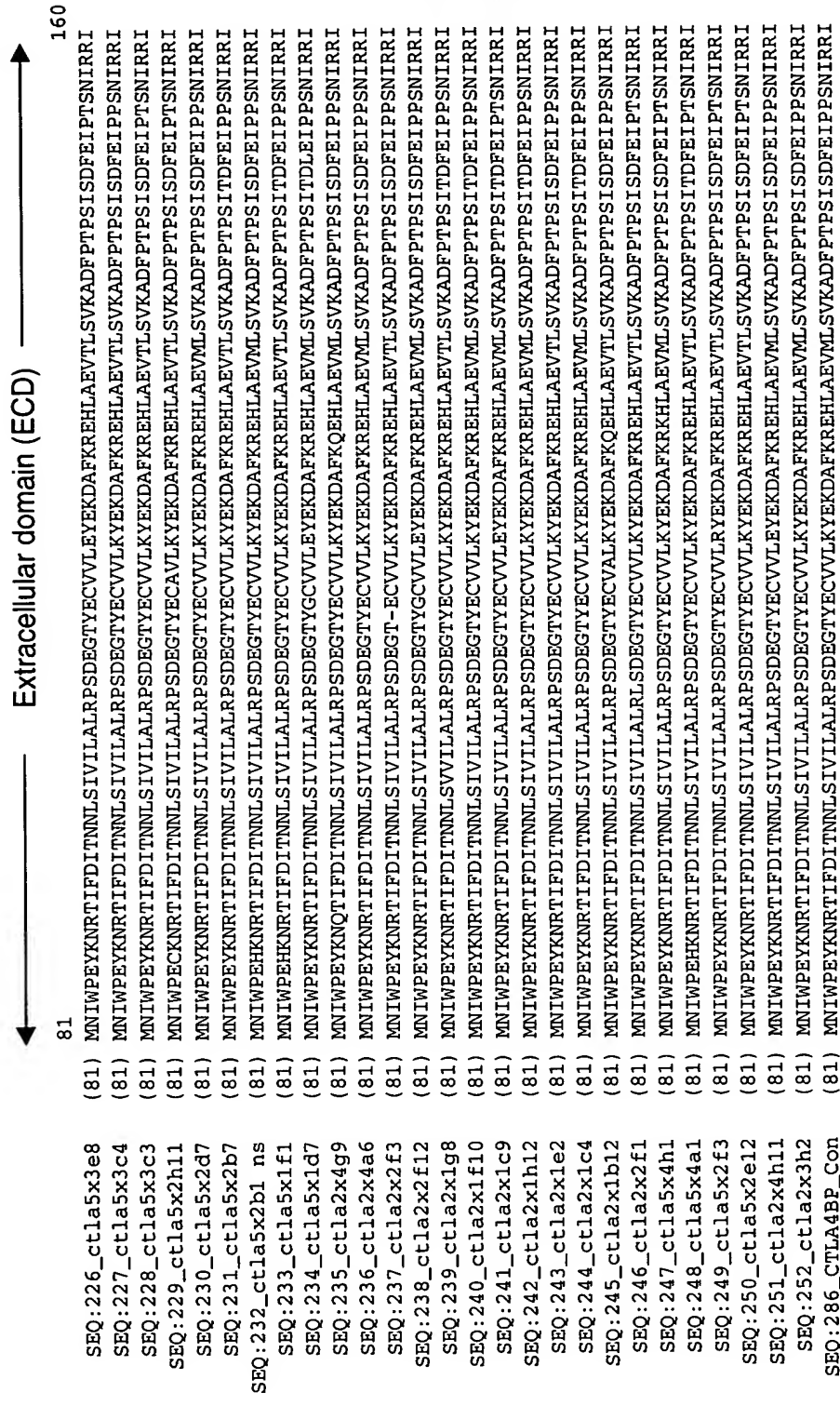


Fig. 3D

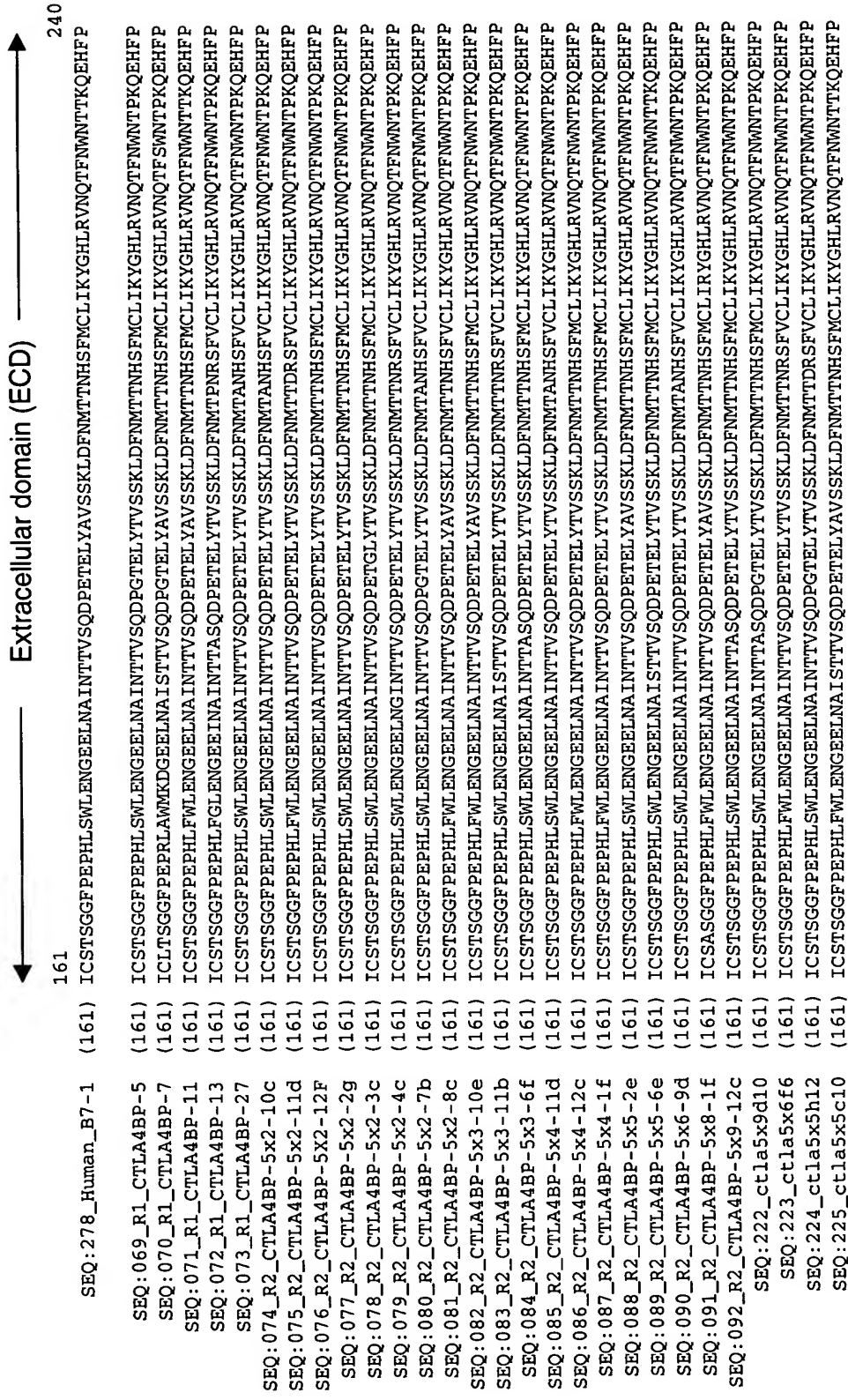


Fig. 3E

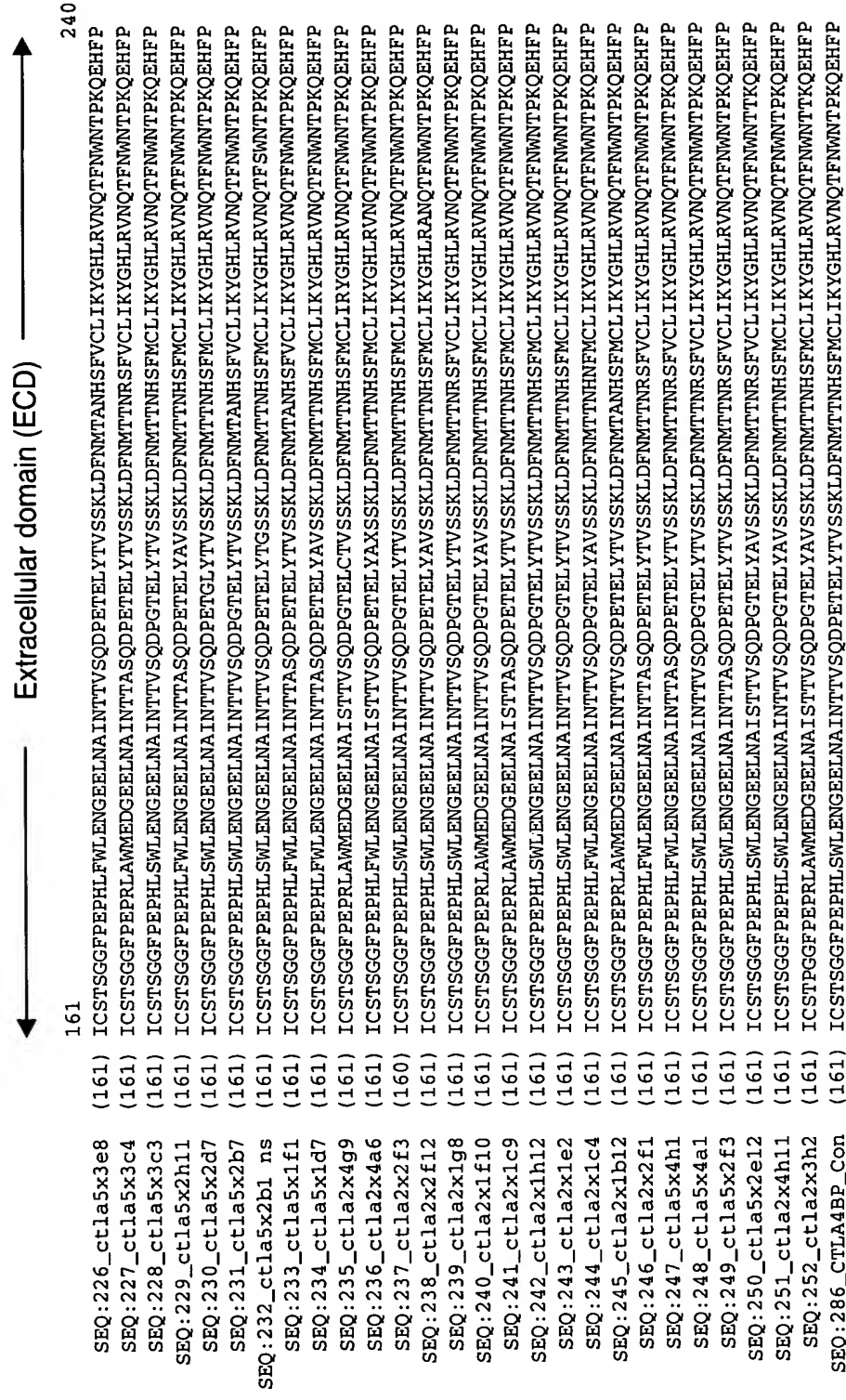


Fig. 3F

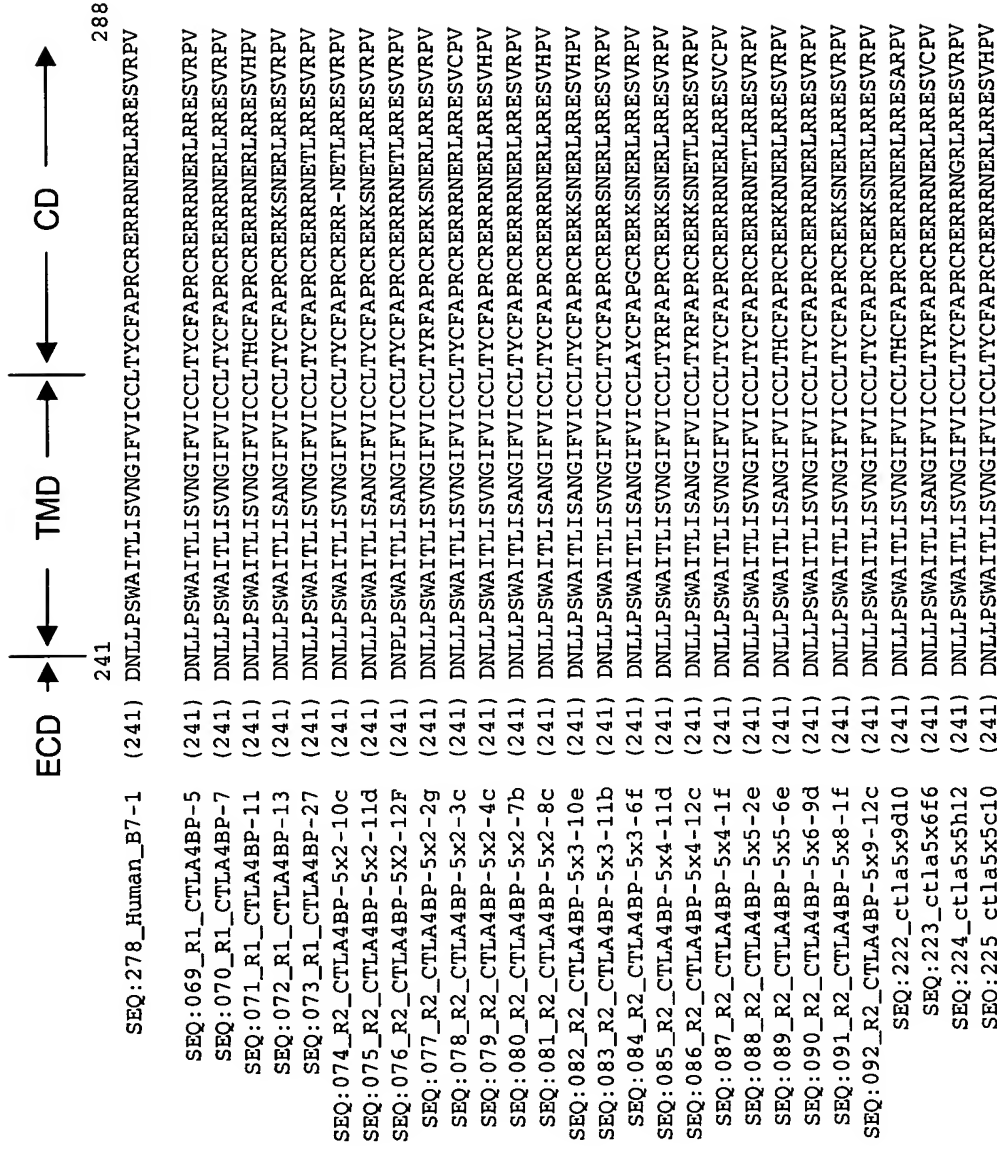


Fig. 3G

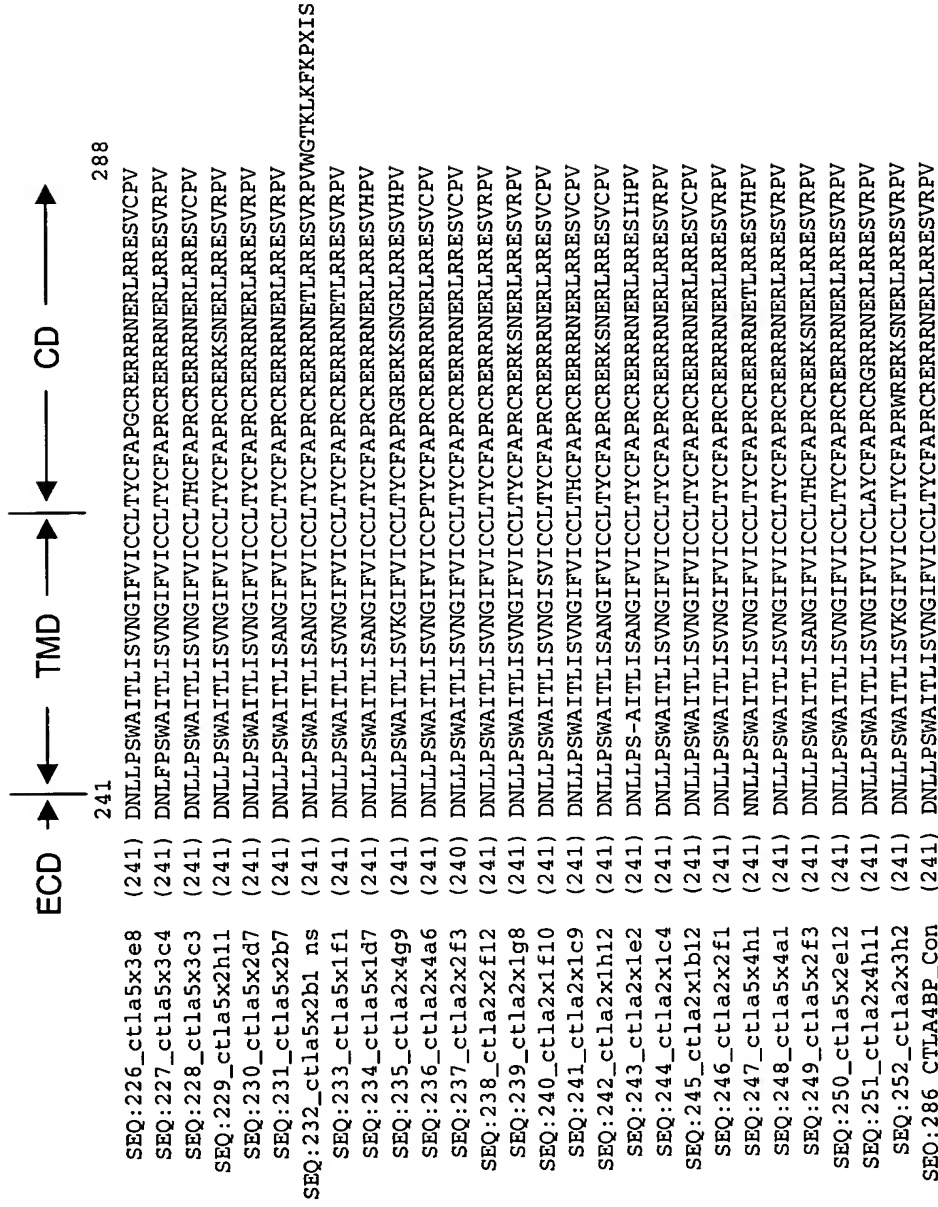


Fig. 3H

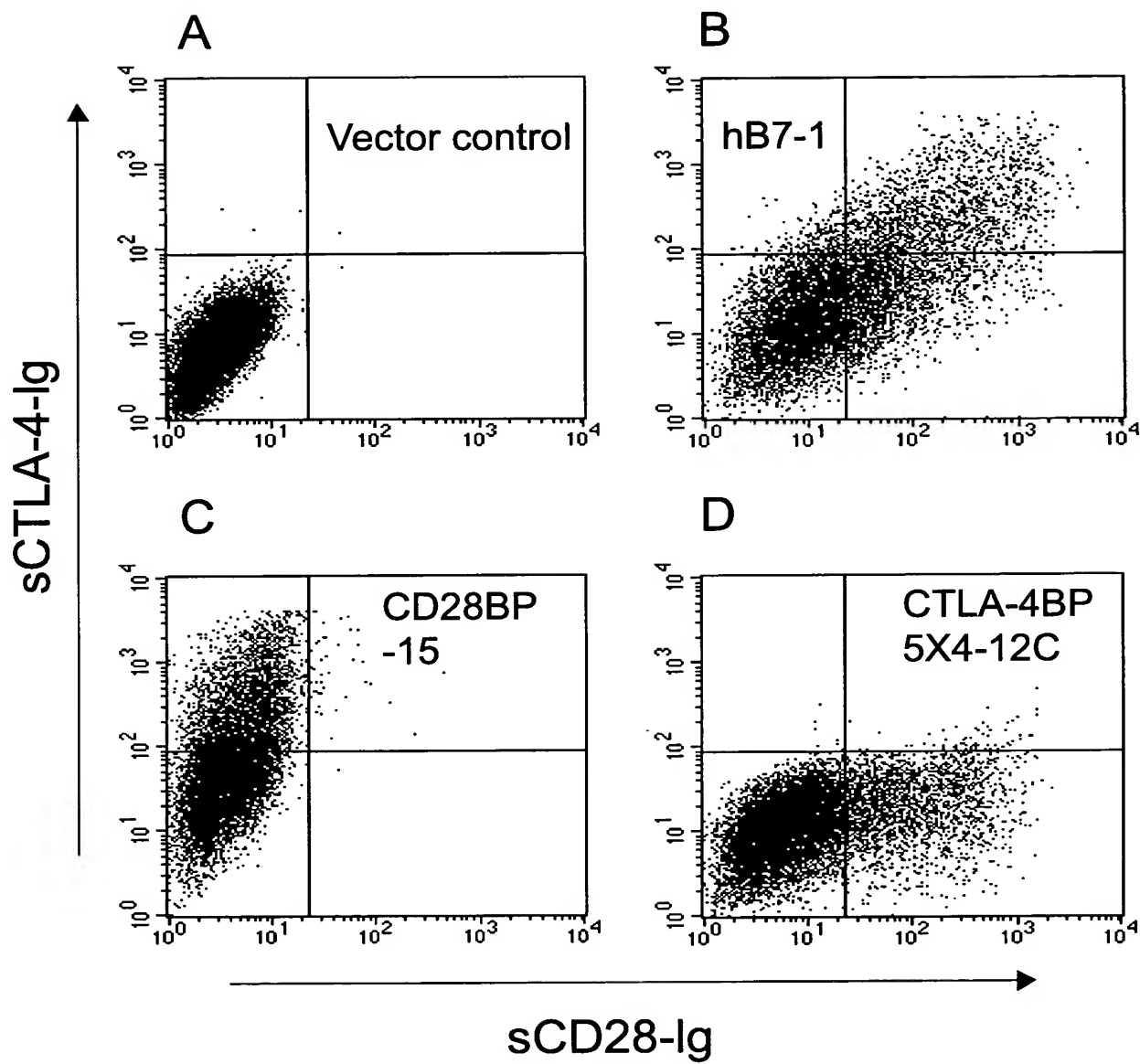


Fig. 4

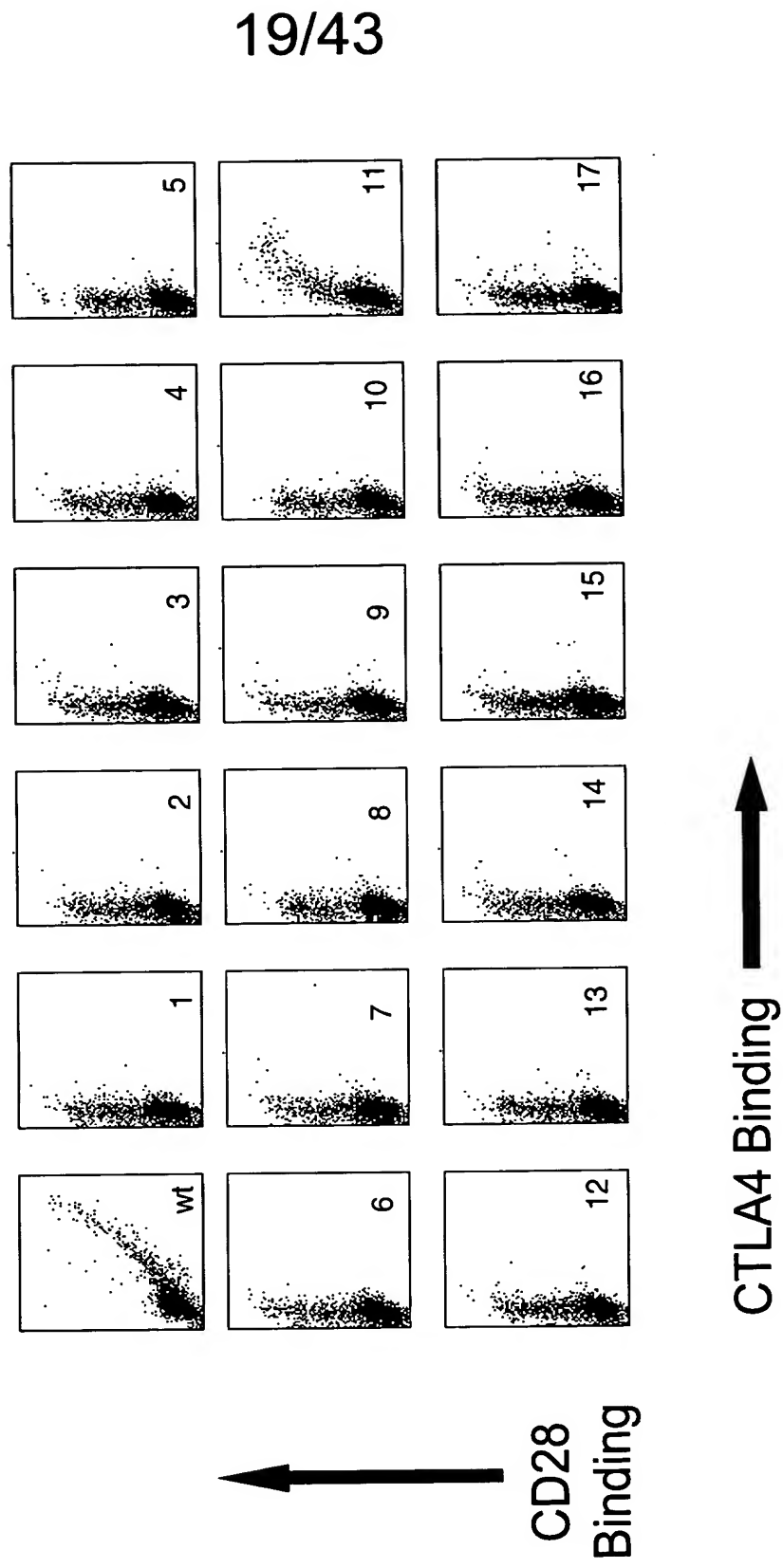
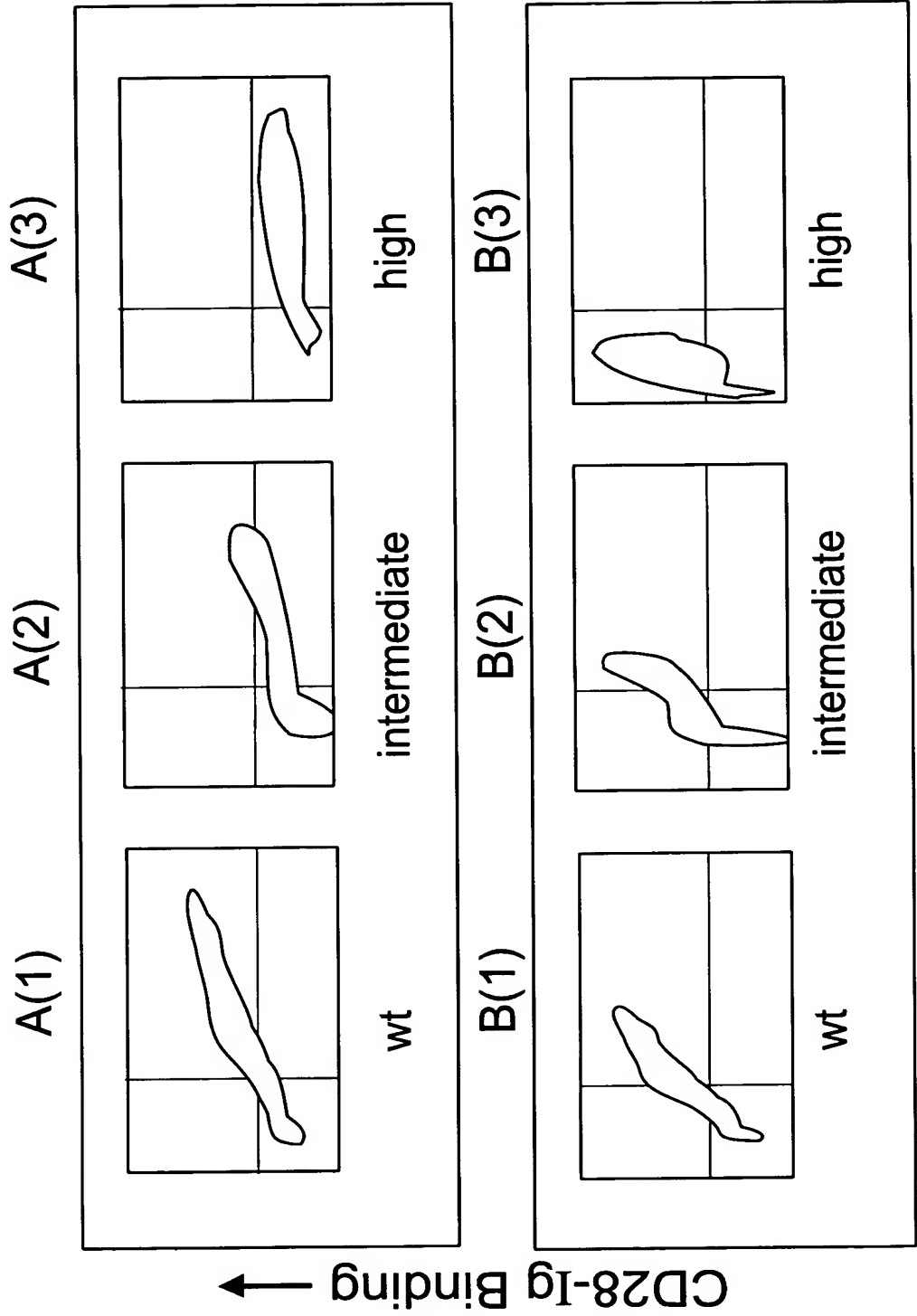


Fig. 5



CTLA-4-Ig Binding →

Fig. 6

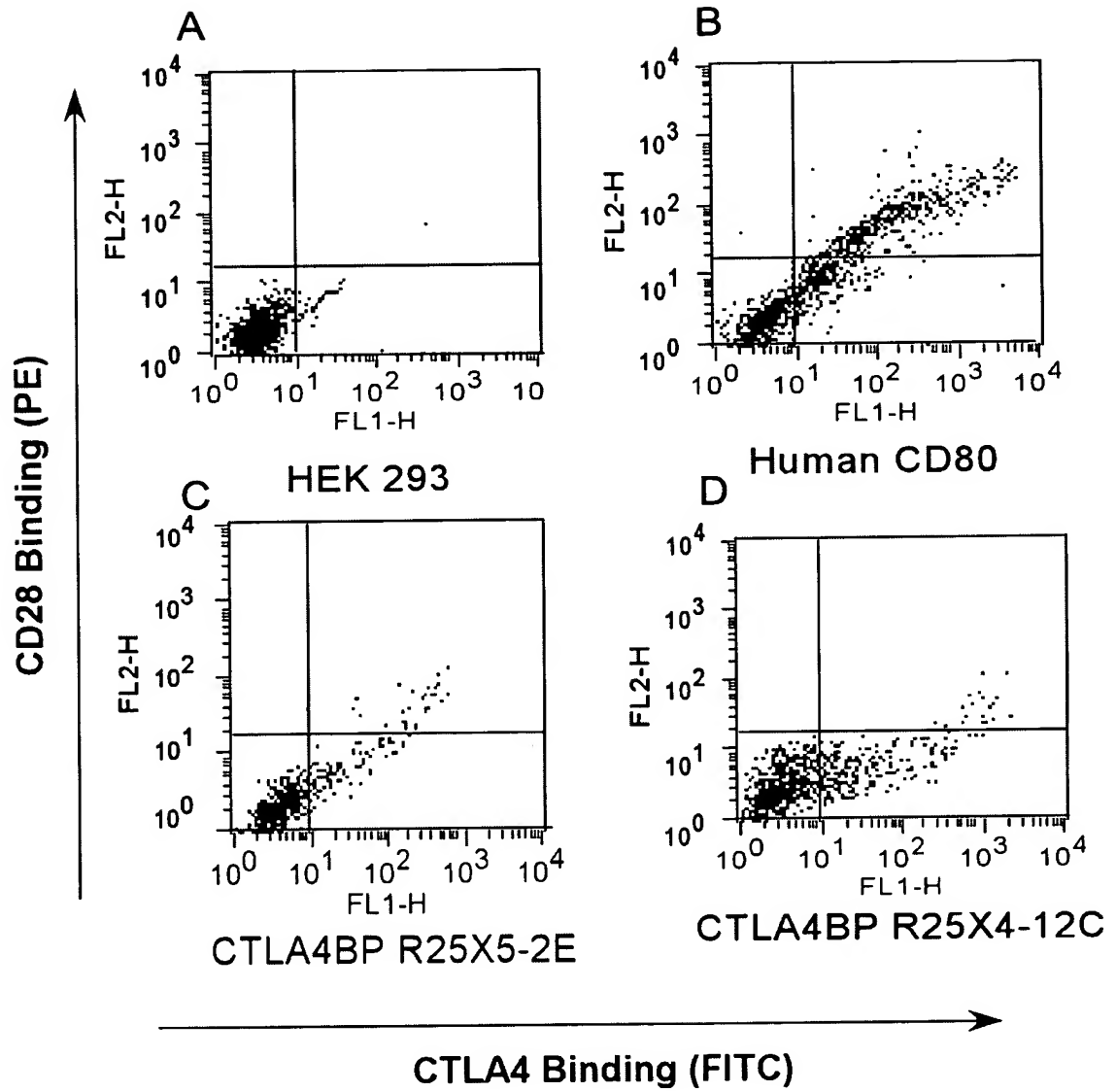


Fig. 7A-D

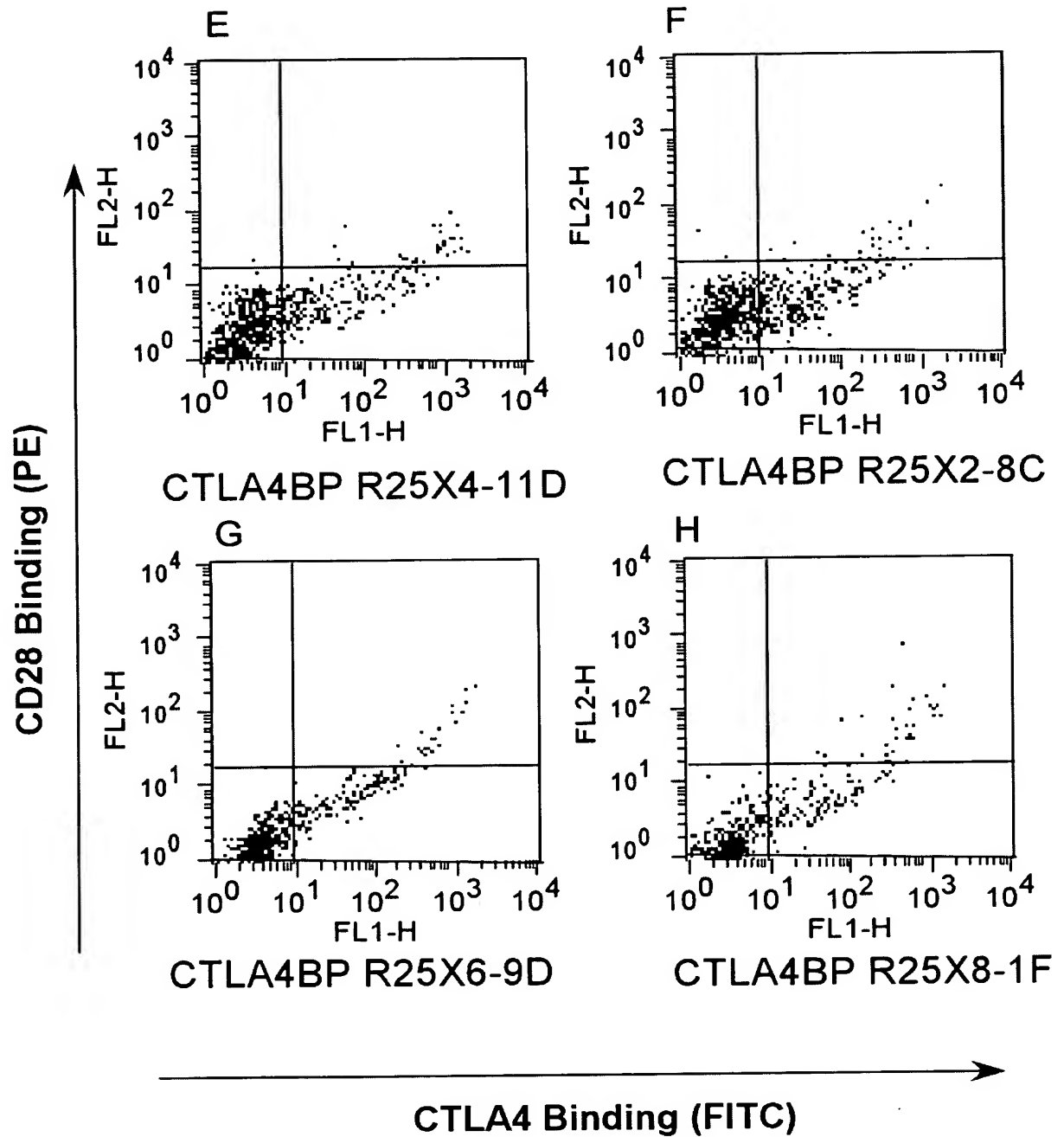


Fig. 7E-H

Fig. 8A

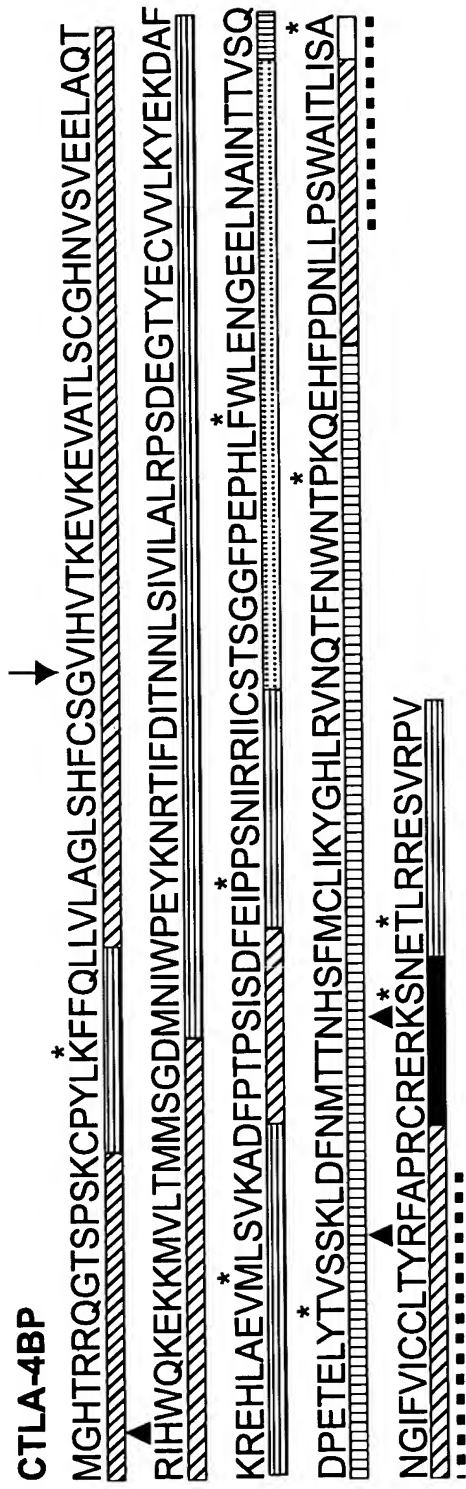
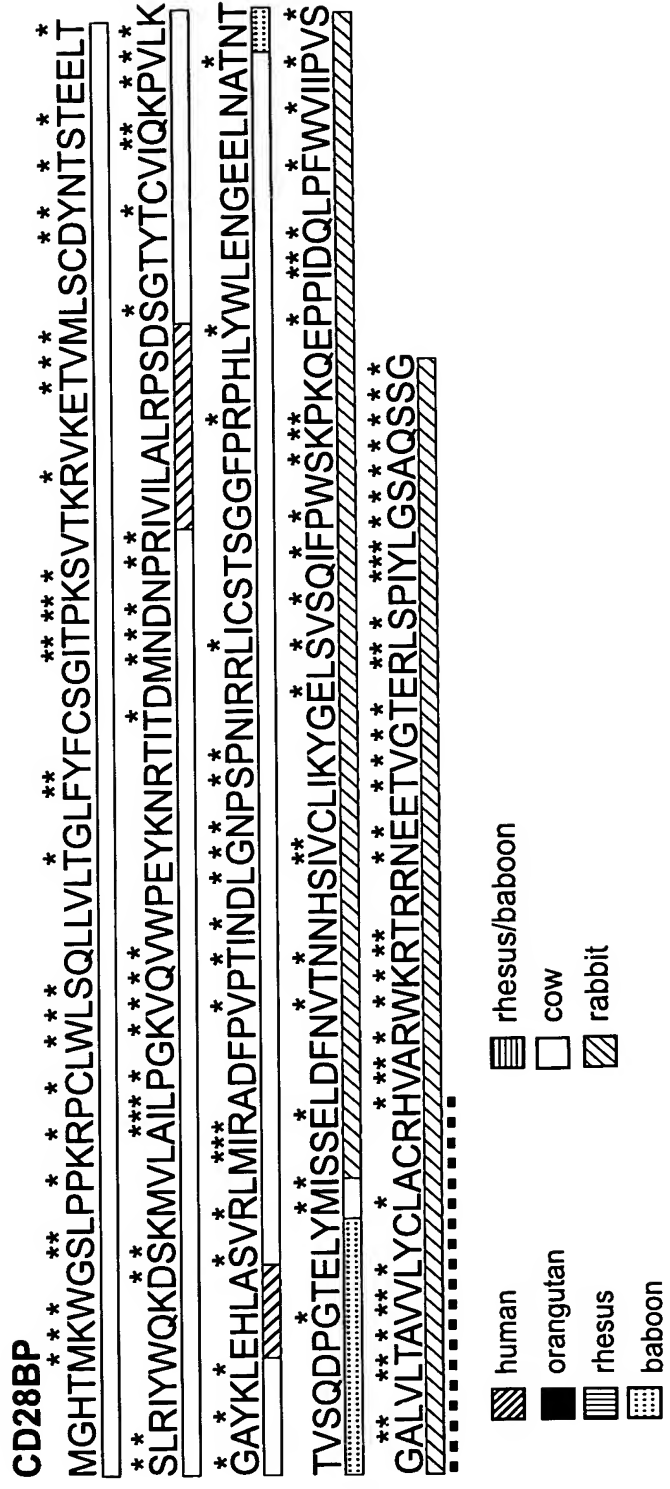
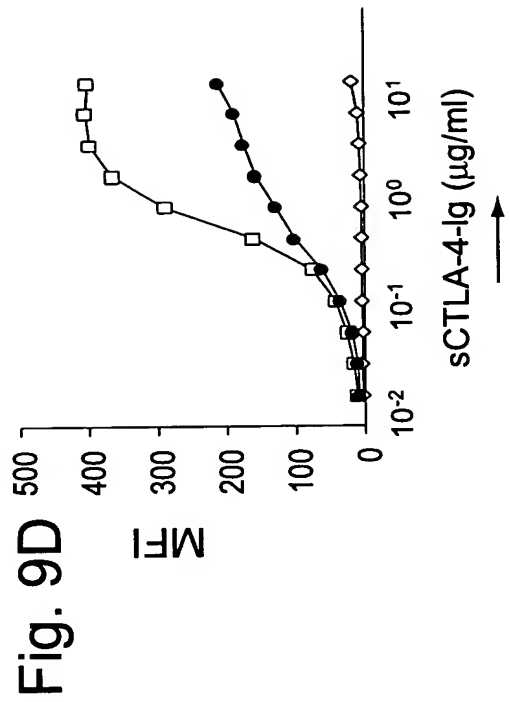
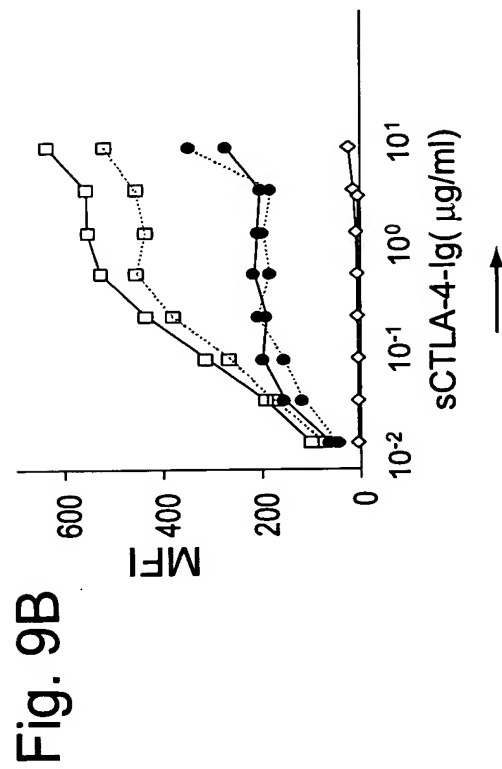
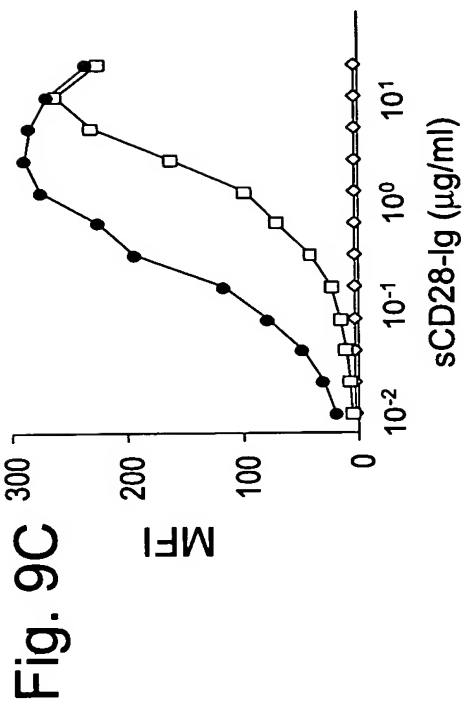
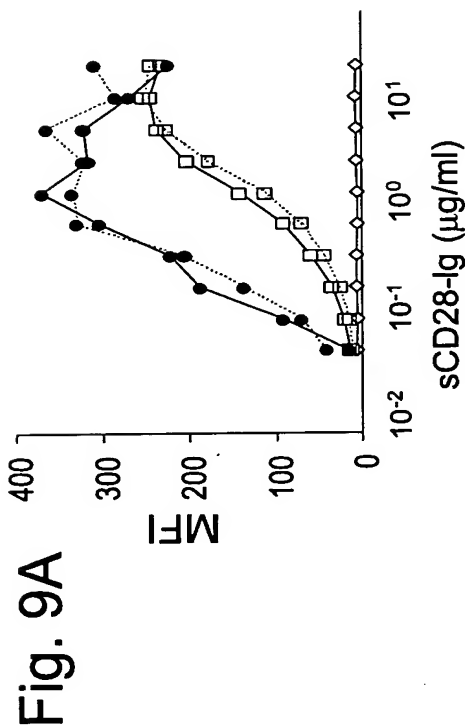


Fig. 8B



- ◇ Vector control
- hB7-1
- ▨ hB7-1-Flag
- CD28BP-15
- CD28BP-Flag
- ▲ CTLA-4BP 5X4-12c



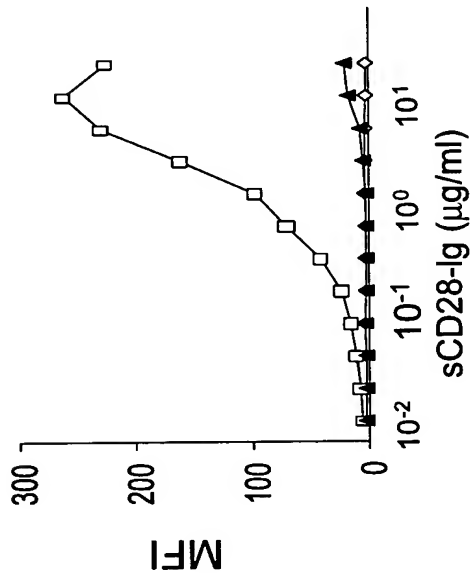
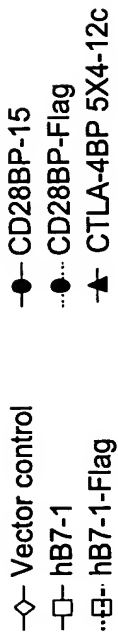


Fig. 9G

MFI

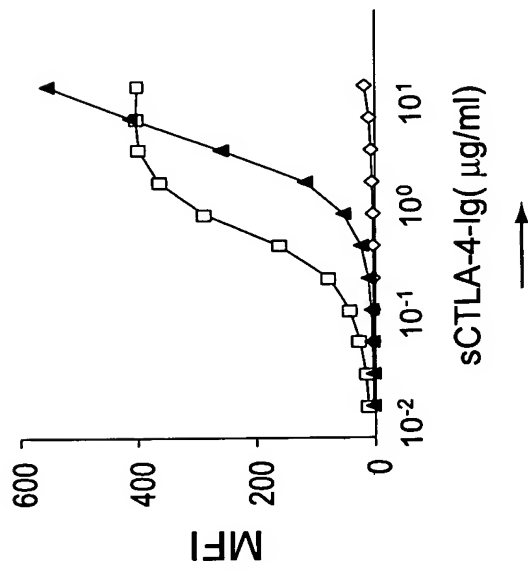
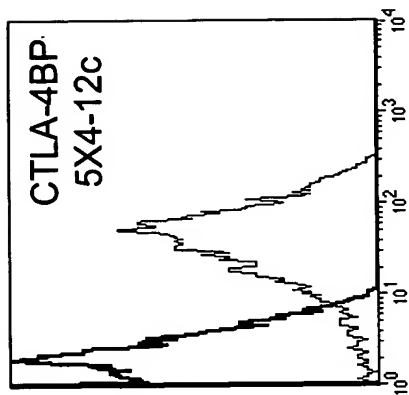
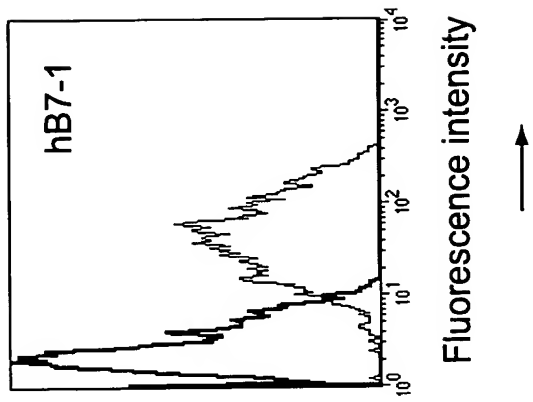


Fig. 9H

MFI



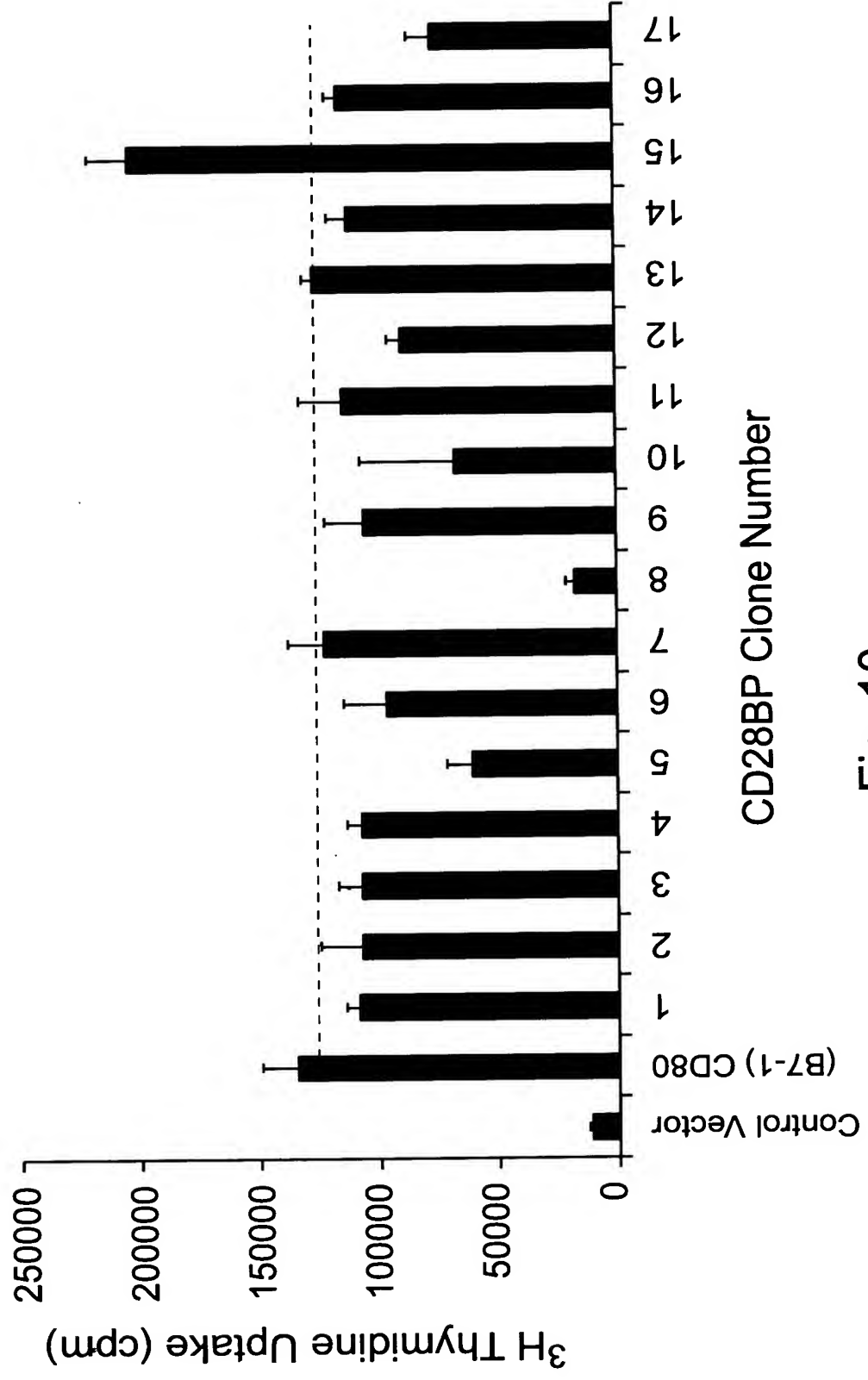


Fig. 10

Fig. 11A

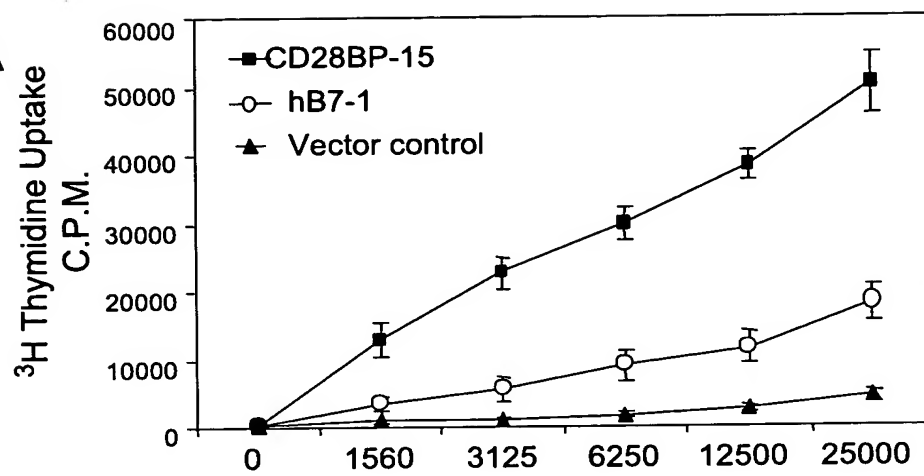


Fig. 11B

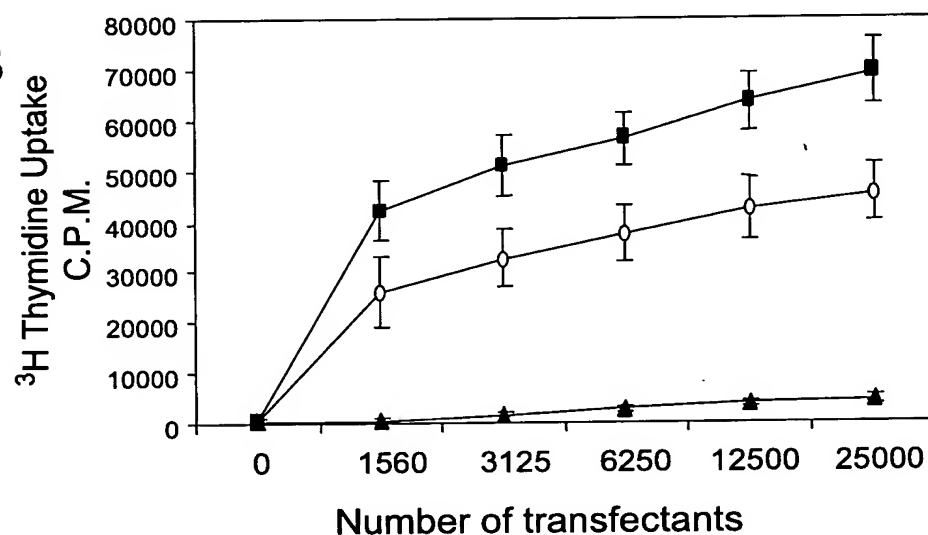
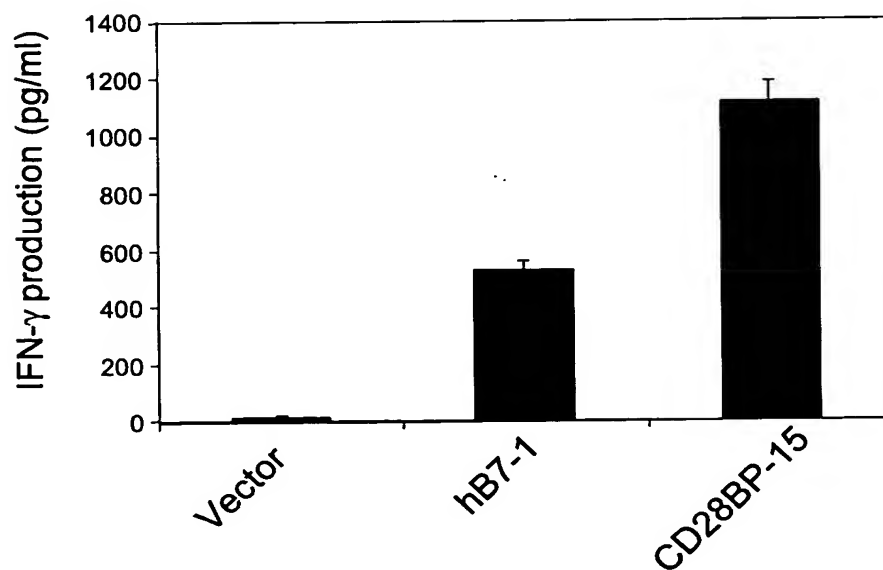


Fig. 11C



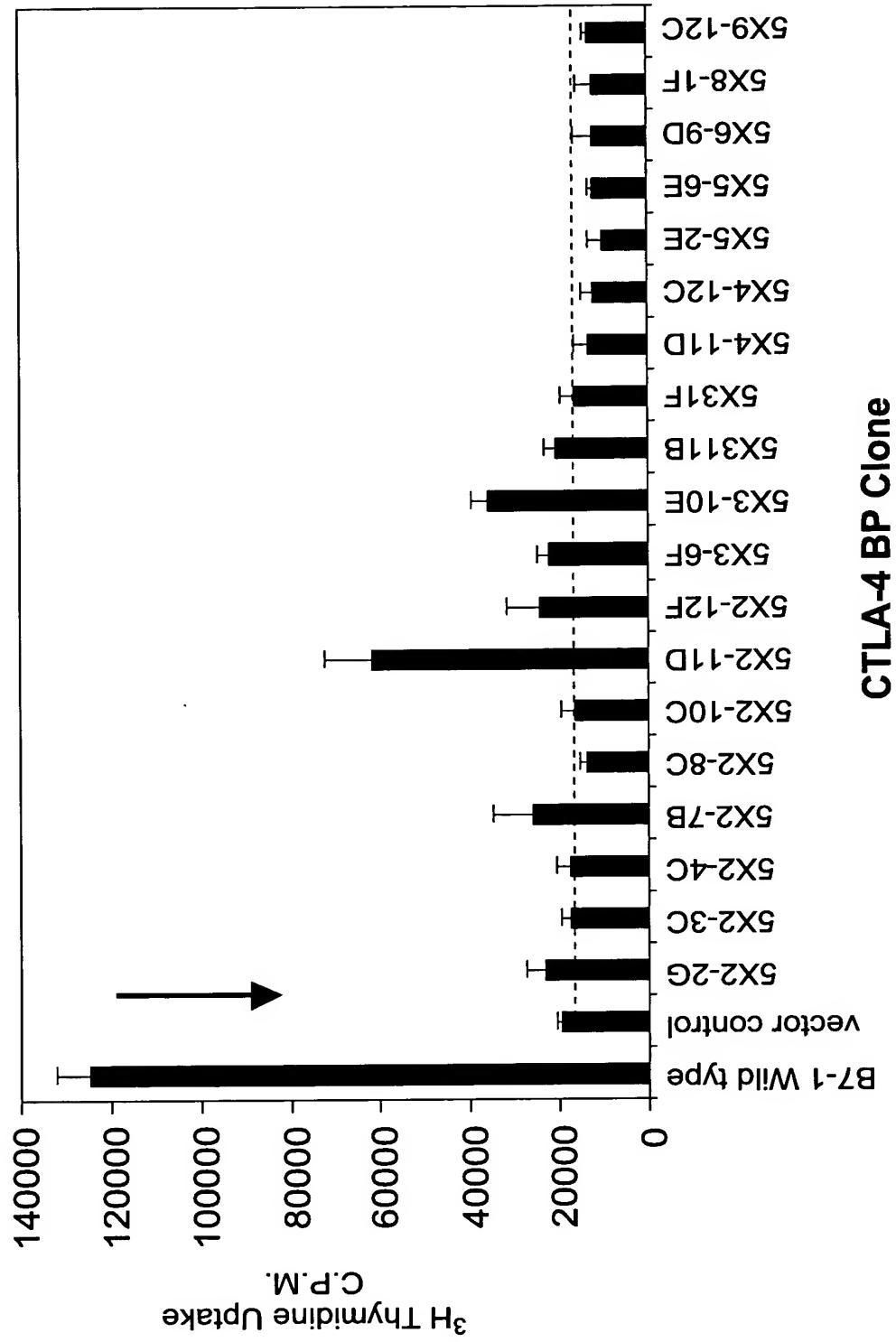


Fig. 12

Fig. 13A

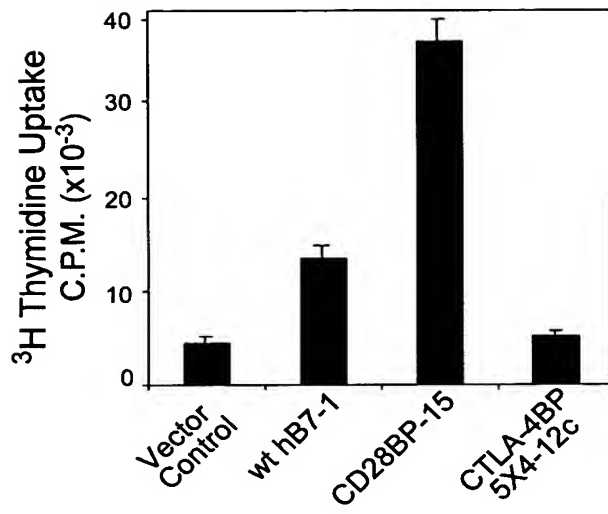


Fig. 13B

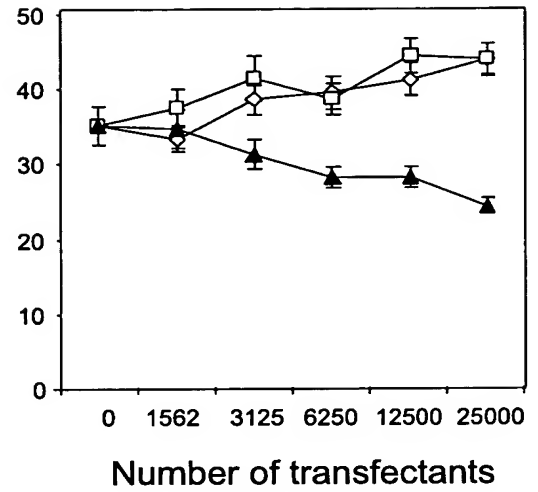


Fig. 13C

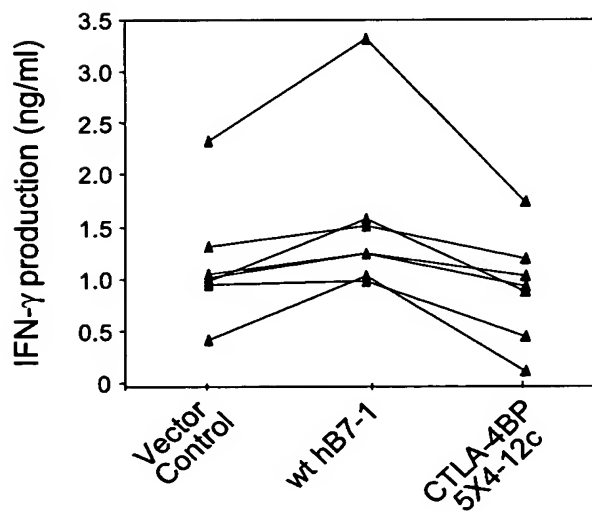


Fig. 13D

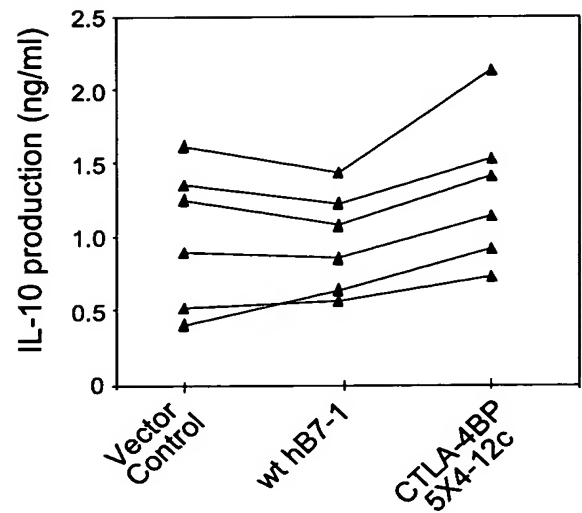


Fig. 14A

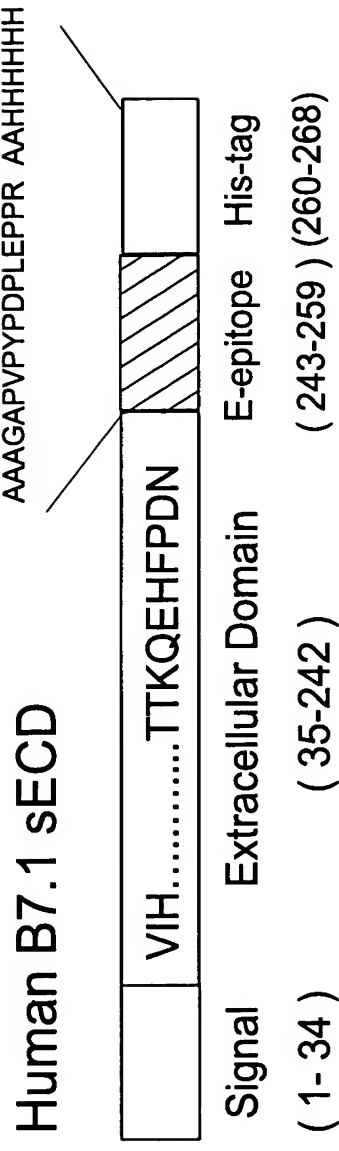
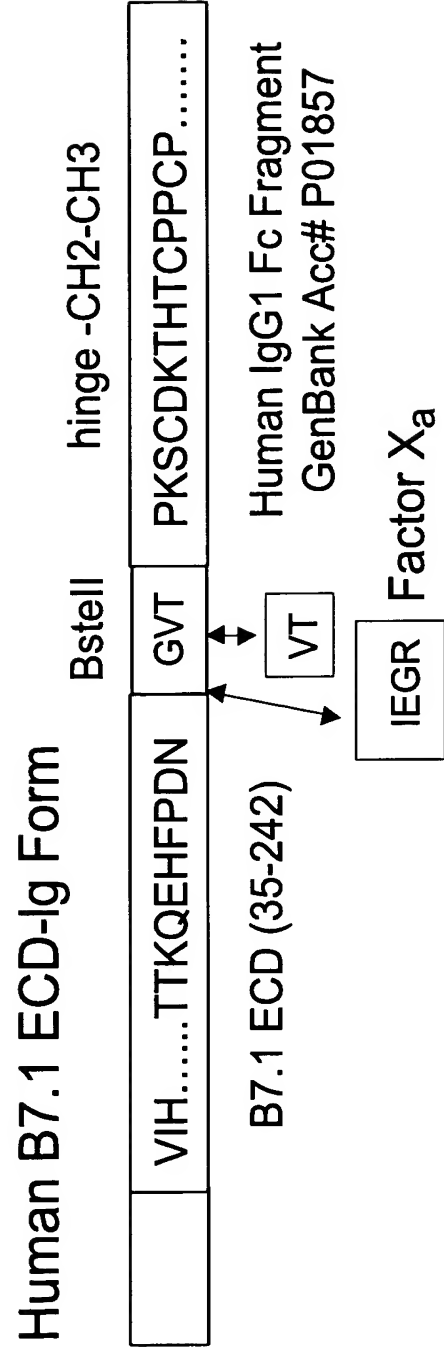


Fig. 14B



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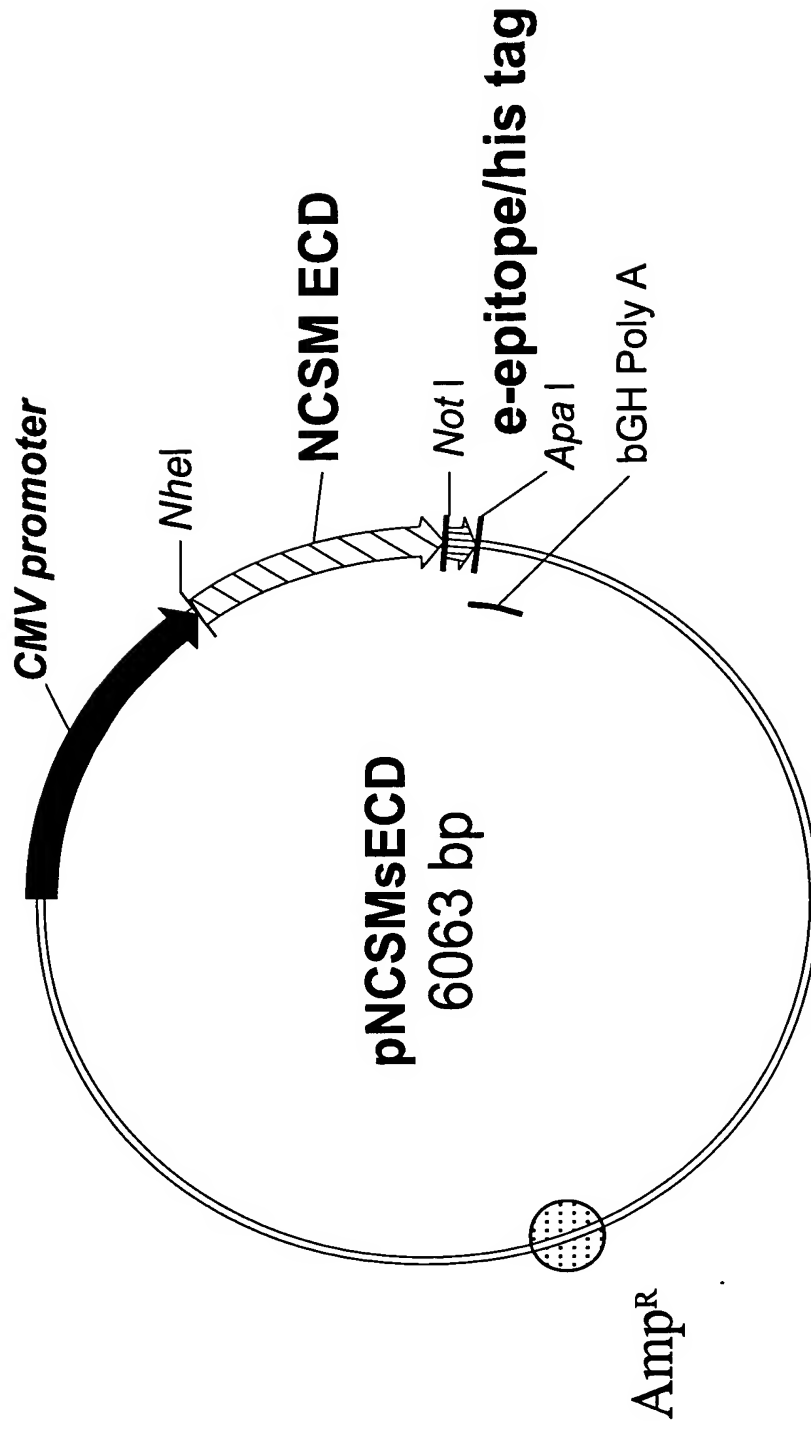


Fig. 15

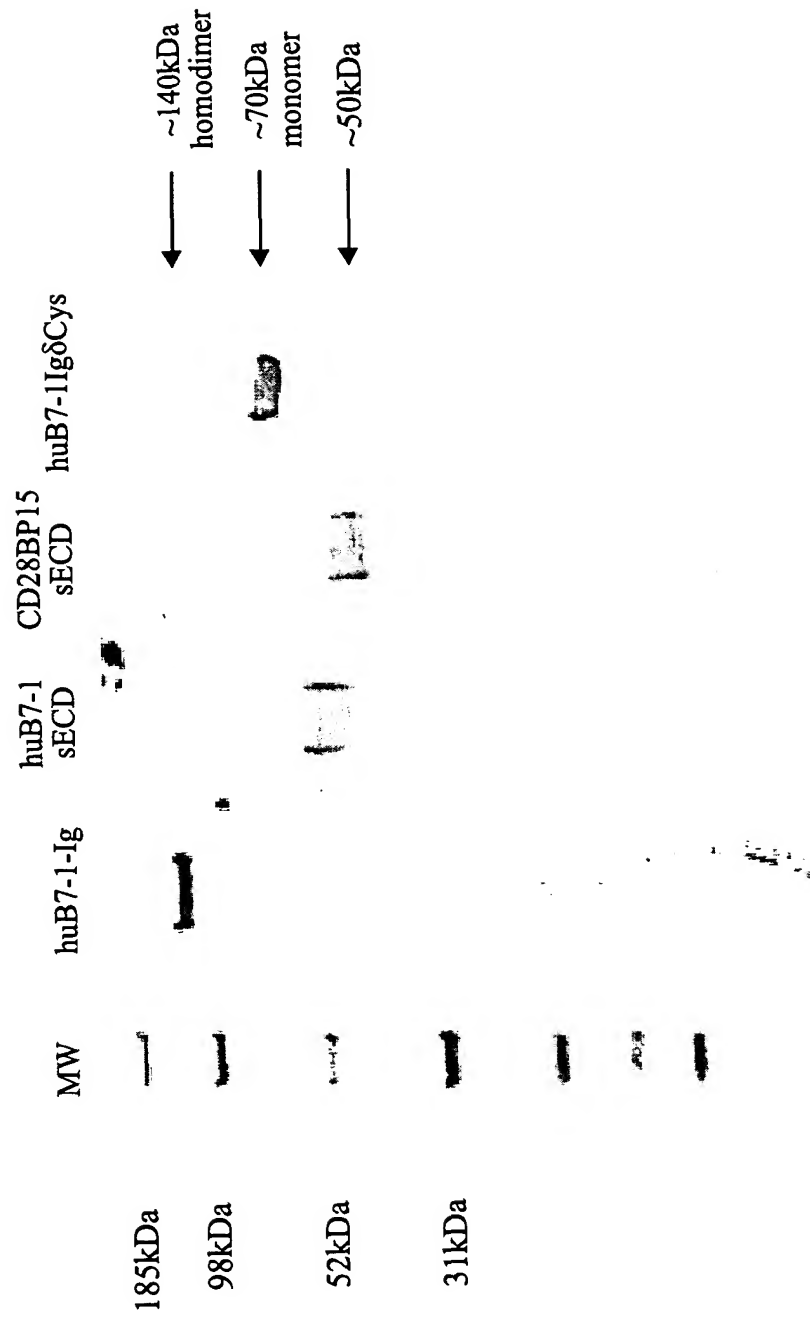


Fig. 16

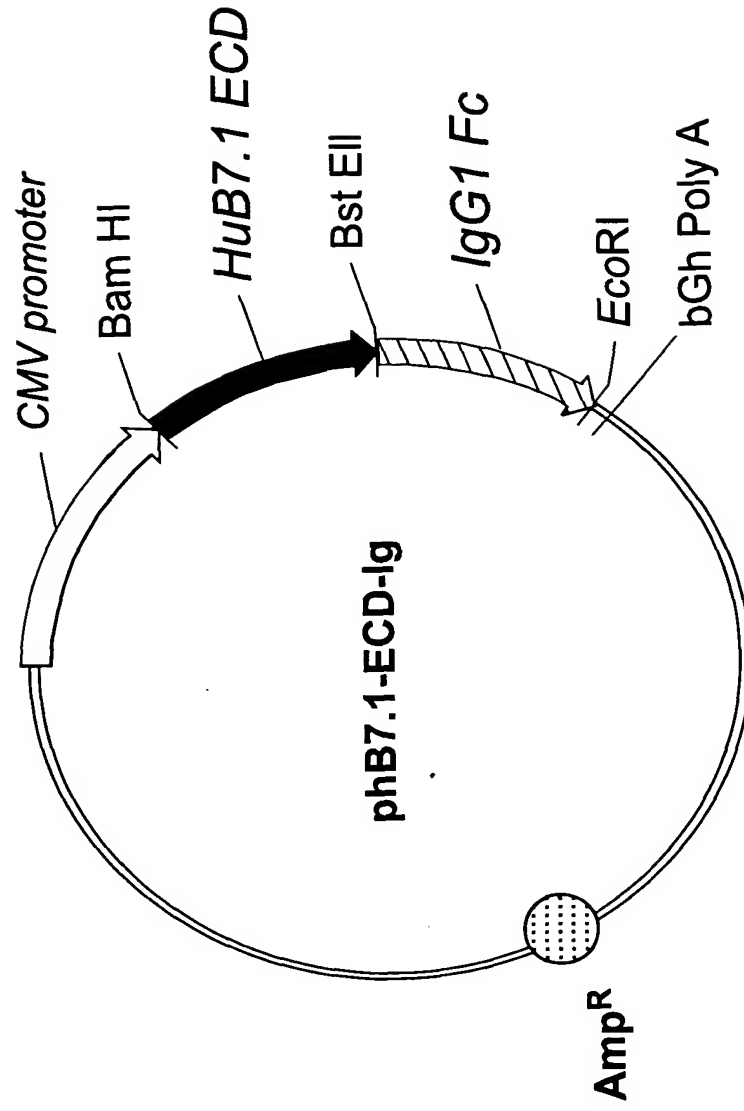


Fig. 17

TF002217 "TF002207"

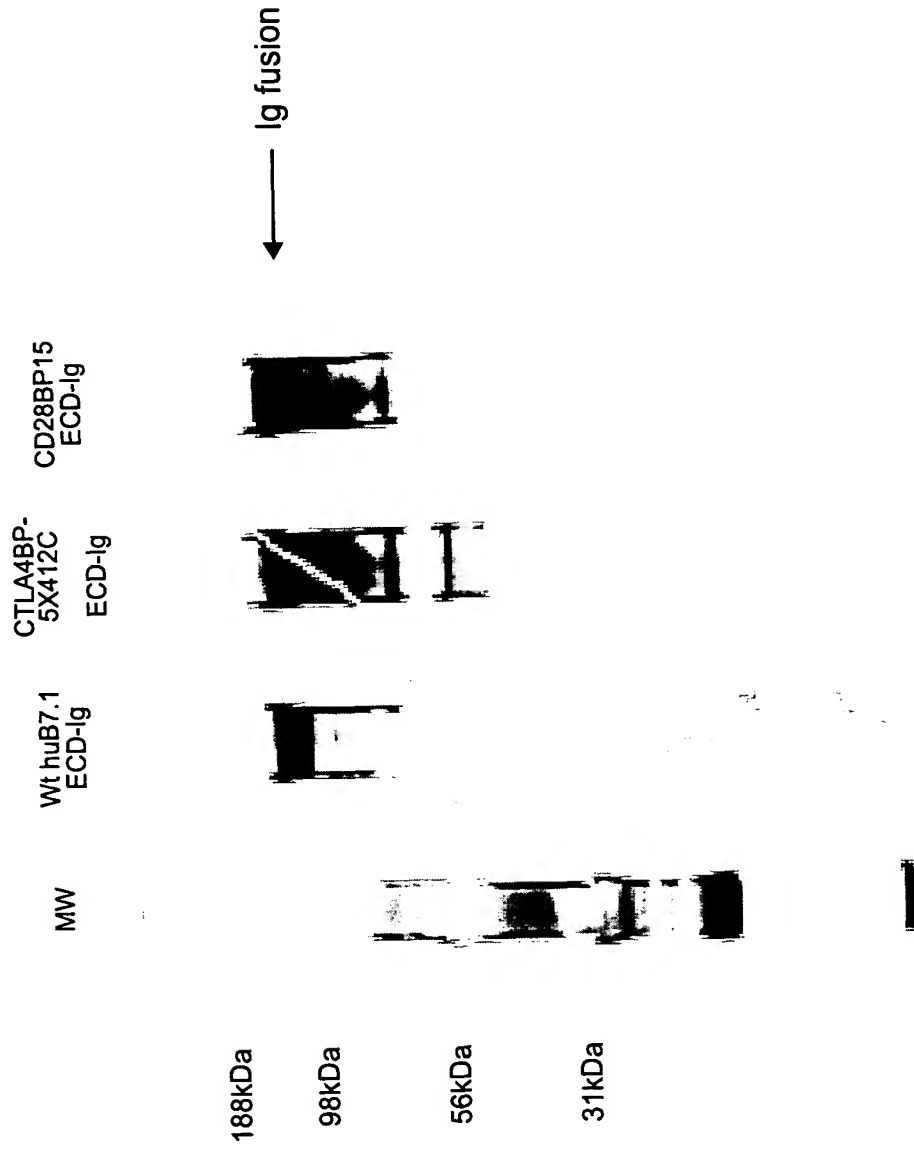


Fig. 18

Expression of CTLA-4BP-Ig and CD28BP-Ig Proteins

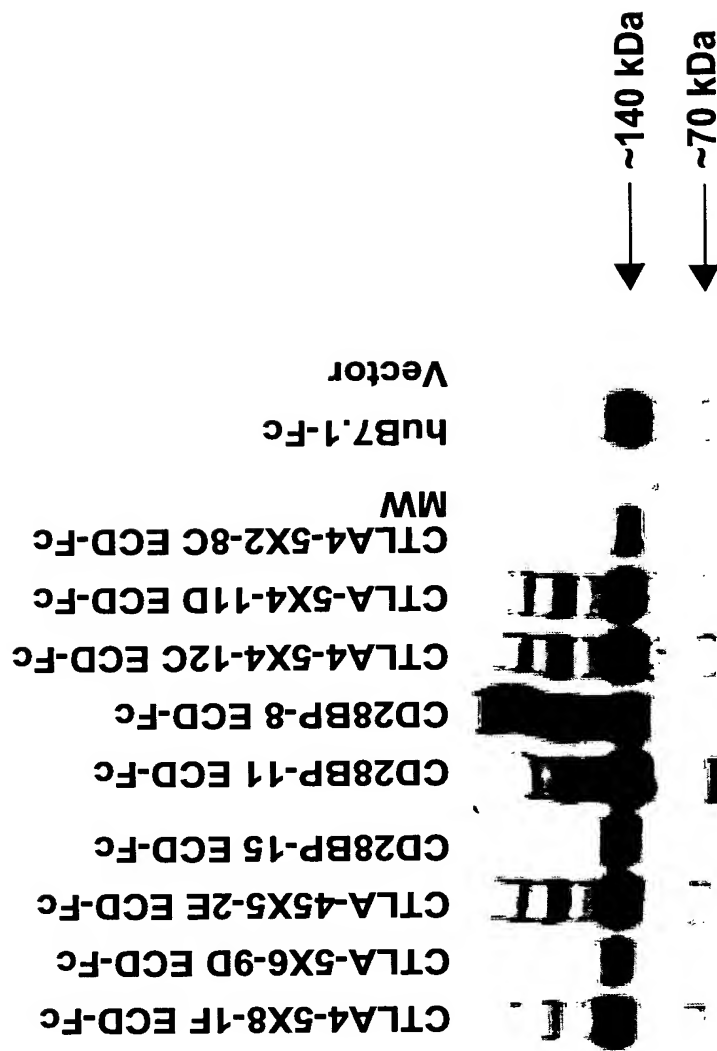


Fig. 19

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Fig. 20A

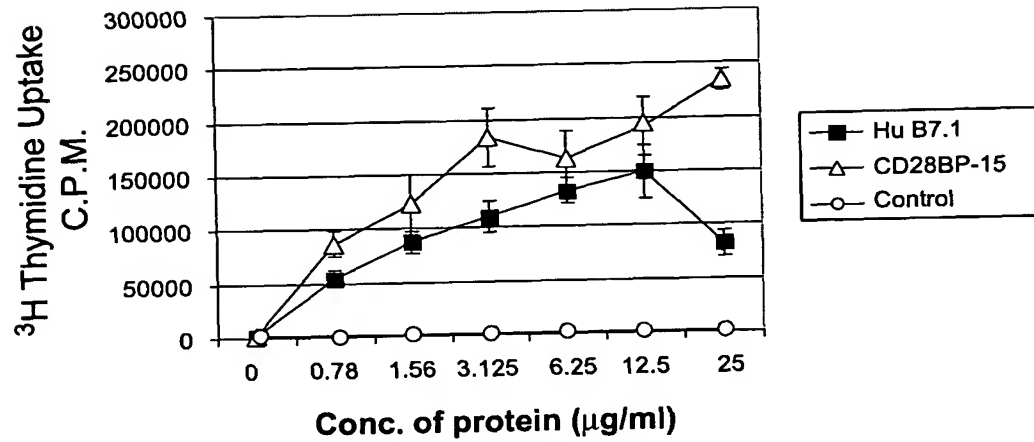
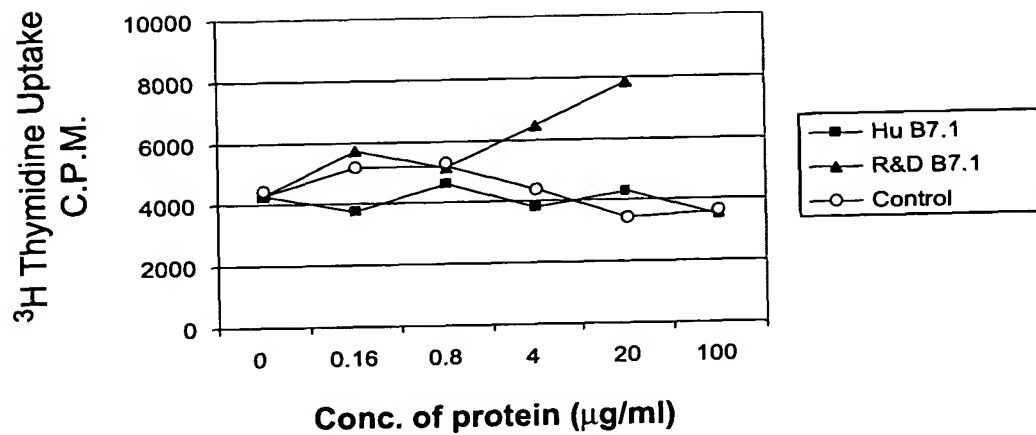


Fig. 20B



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Fig. 20C

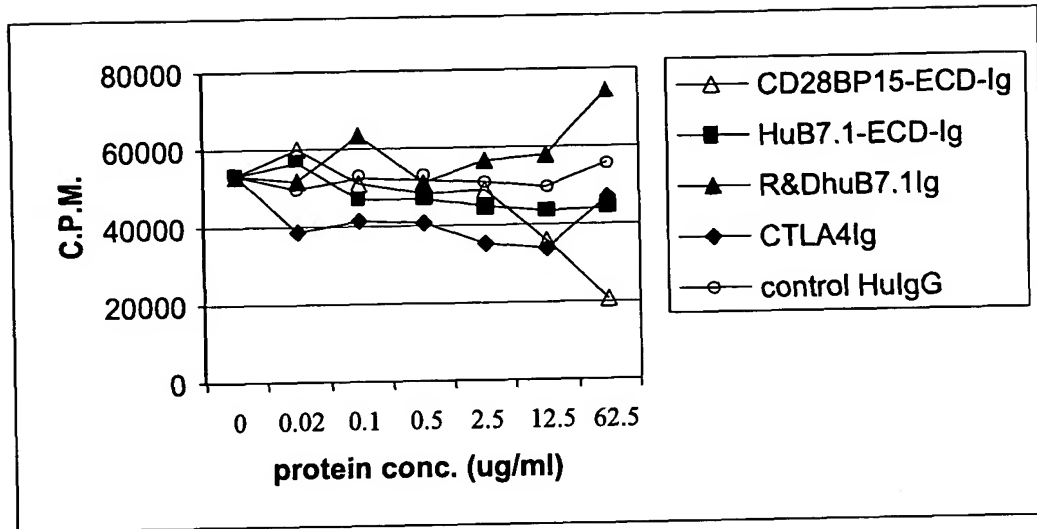
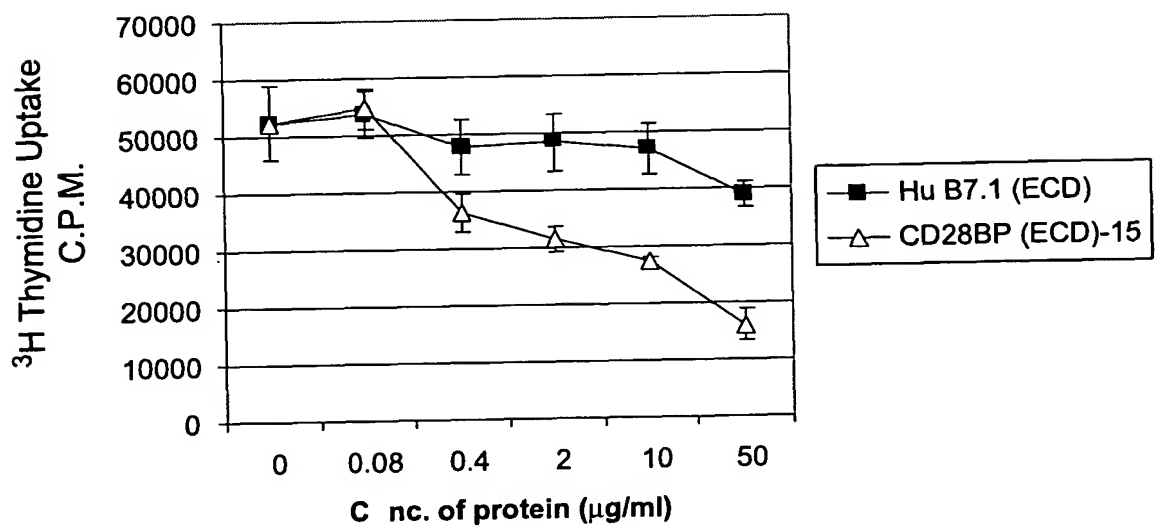


Fig. 20D



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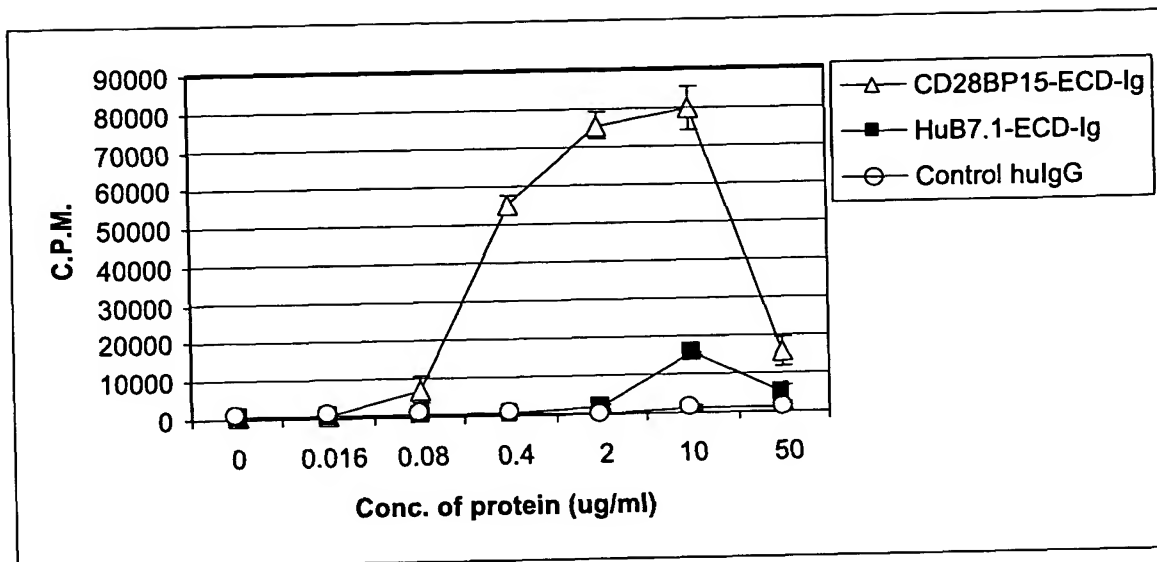


Fig. 20E

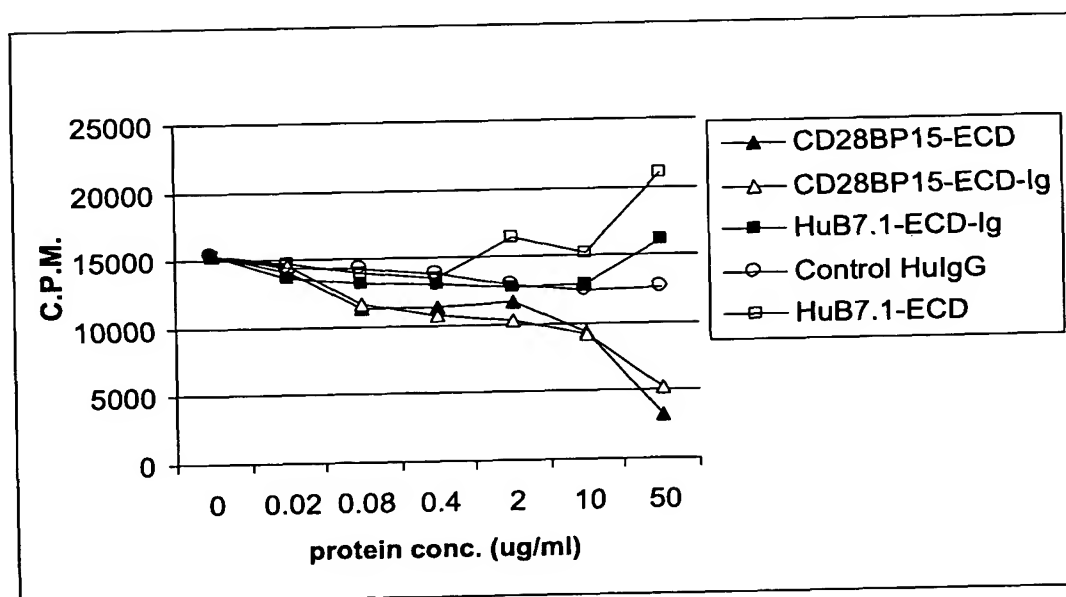


Fig. 20F

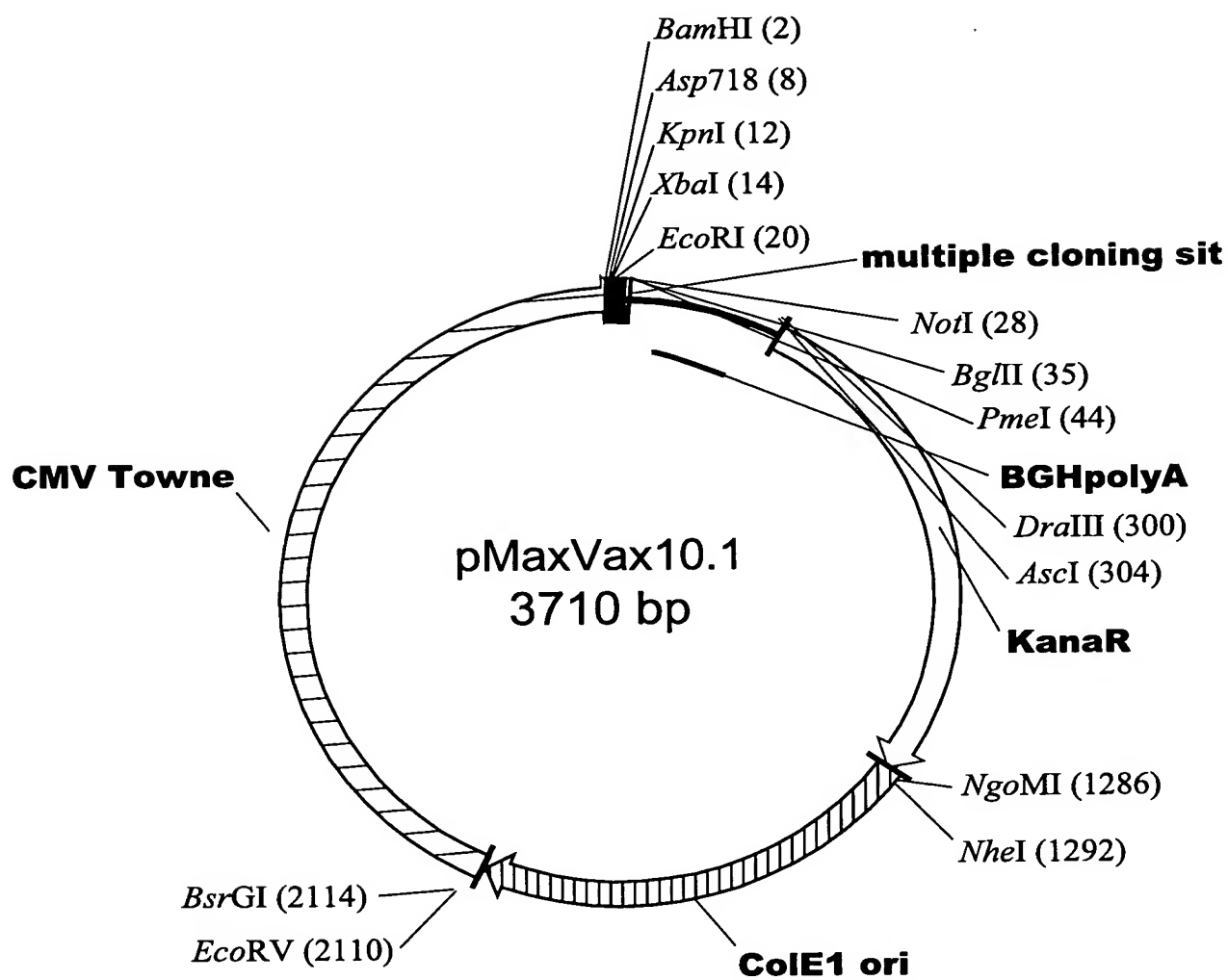


Fig. 21

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Fig. 22A

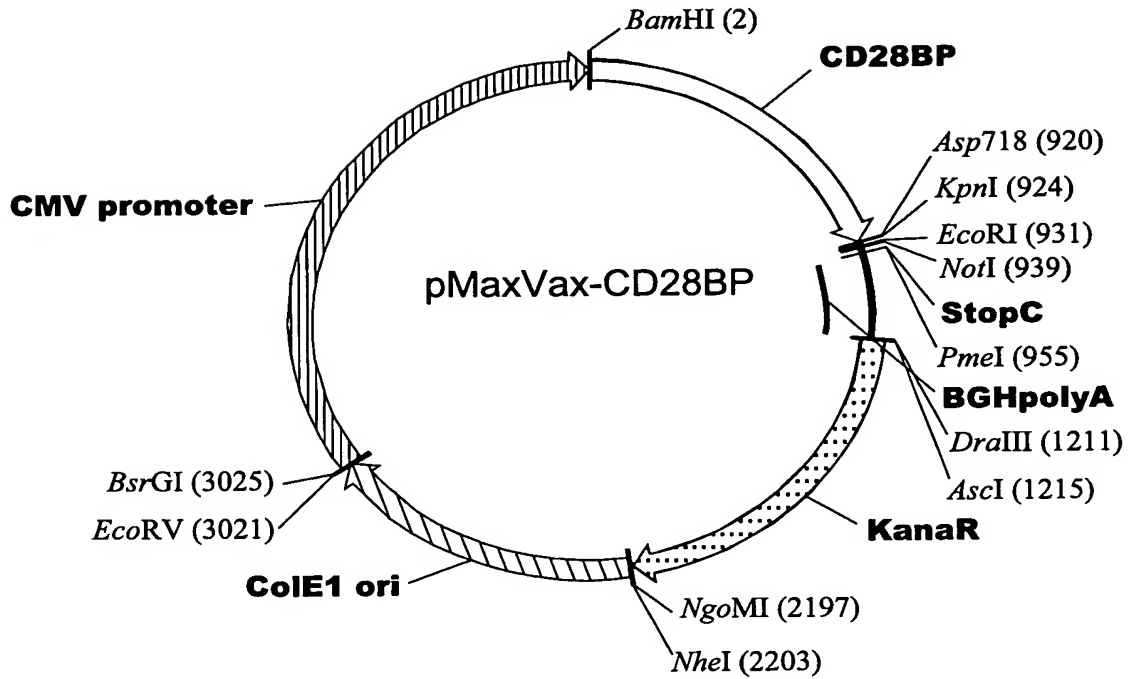
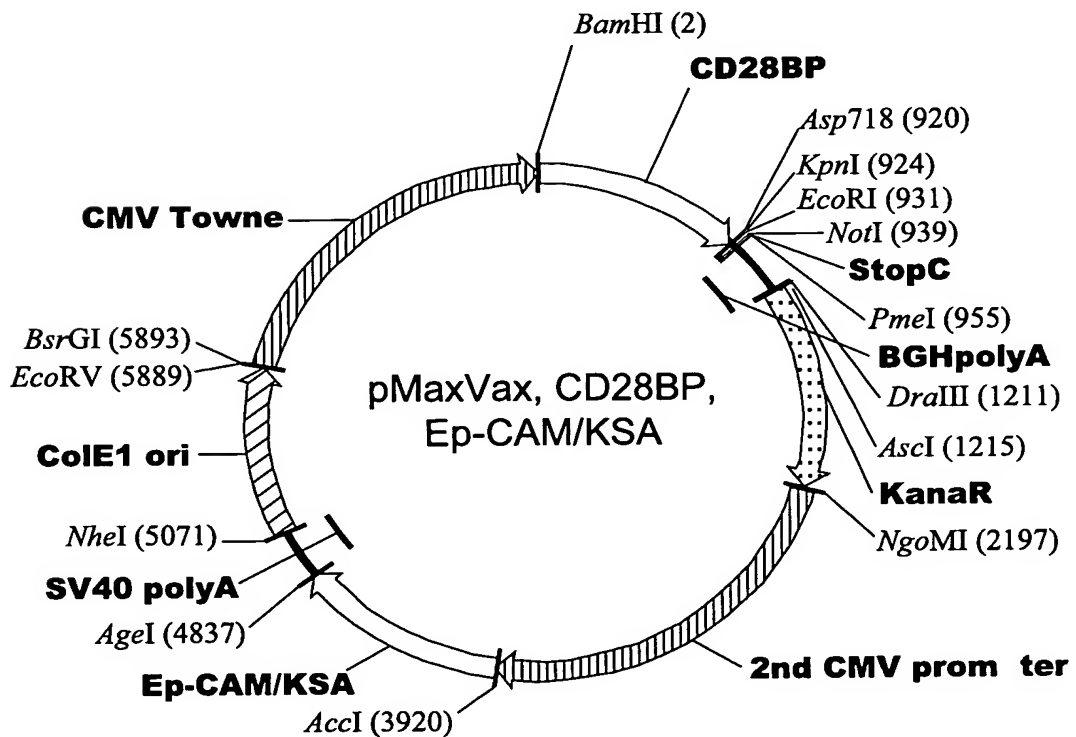


Fig. 22B



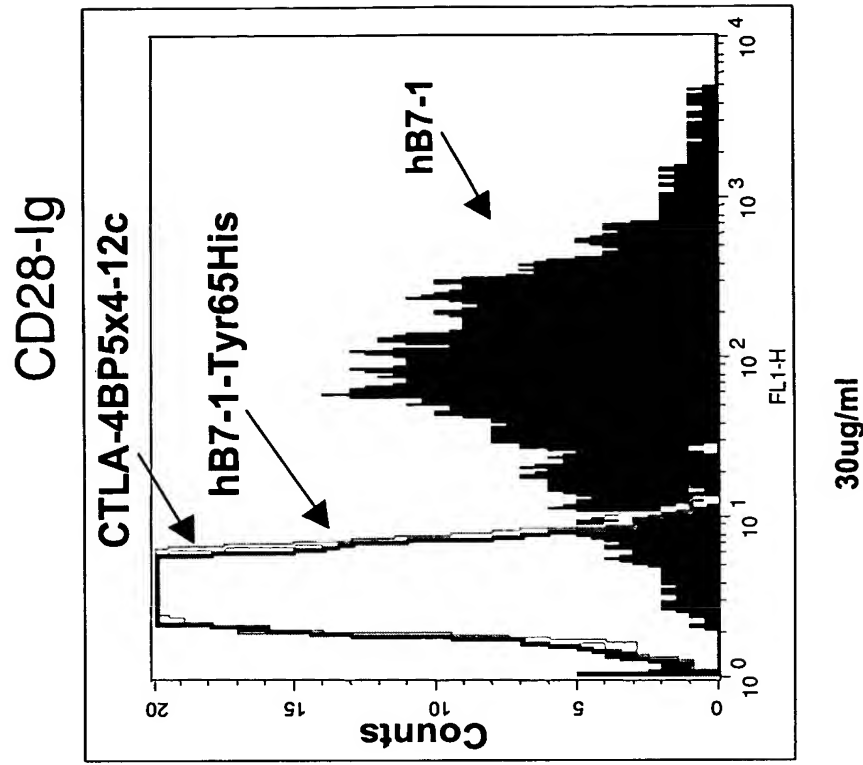


Fig. 23B

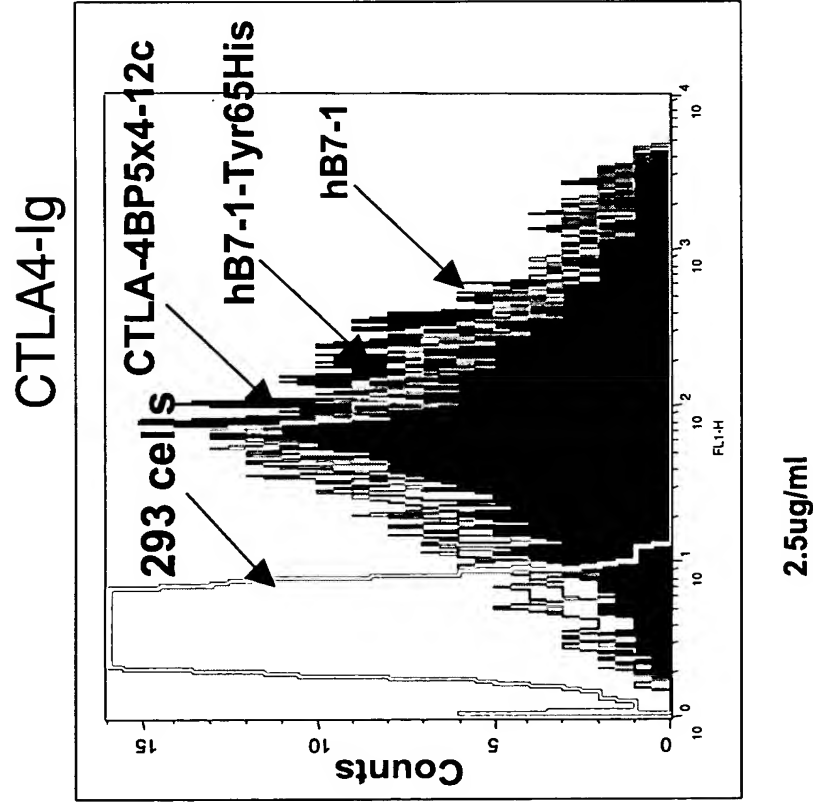


Fig. 23A

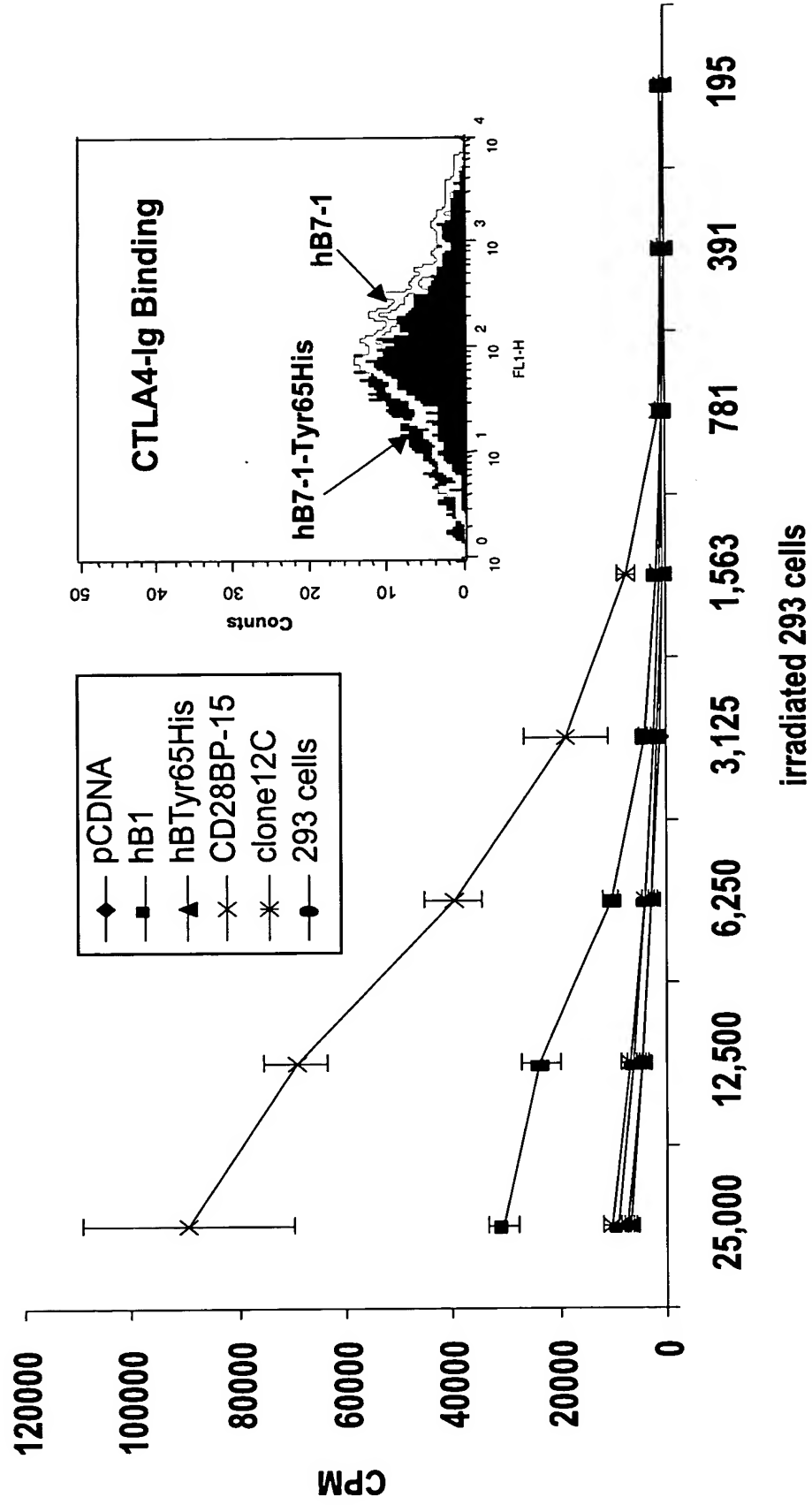


Fig. 24

Fig. 25A

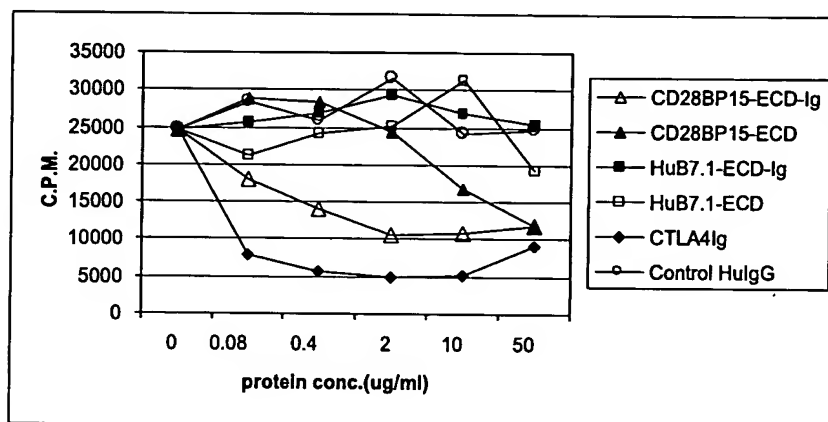


Fig. 25B

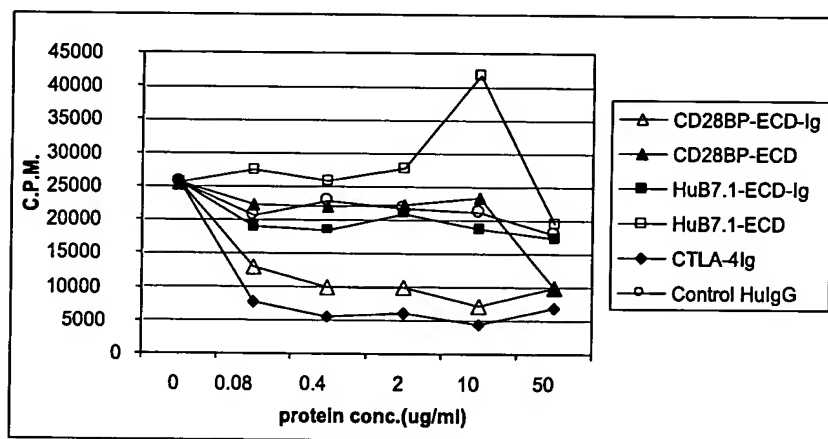


Fig. 25C

